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(54) Title: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS			
(57) Abstract			
Described herein are methods that can be used for diagnosis and prognosis of colorectal cancer. Also described herein are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, methods and molecular targets (genes and their products) for therapeutic intervention in colorectal and other cancers are described.			

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NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR COLORECTAL CANCER MODULATORS

FIELD OF THE INVENTION

5 The invention relates to the identification of expression profiles and the nucleic acids involved in colorectal cancer, and to the use of such expression profiles and nucleic acids in diagnosis and prognosis of colorectal cancer. The invention further relates to methods for identifying and using candidate agents and/or targets which modulate colorectal cancer.

BACKGROUND OF THE INVENTION

10 Colorectal cancer is a significant cancer in Western populations. It develops as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a
15 tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF- β signaling pathway. For a review, see Molecular Biology of Colorectal Cancer, pp238-299, in Curr. Probl. Cancer, Sept/Oct 1997.

20 Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, dissemination of tumor cells (metastases) to locoregional lymph nodes is an important prognostic factor; five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases
25 can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast

majority of colorectal cancers but not in normal tissues. Liefers et al., New England J. of Med. 339(4):223 (1998).

Thus, methods that can be used for diagnosis and prognosis of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of colorectal cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate colorectal cancer. Additionally, provided herein are molecular targets for therapeutic intervention in colorectal and other cancers.

SUMMARY OF THE INVENTION

The present invention provides methods for screening for compositions which modulate colorectal cancer. Also provided herein are methods of inhibiting proliferation of cell, preferably a colorectal cancer cell. Methods of treatment of cancer, as well as compositions, are also provided herein.

In one aspect, a method of screening drug candidates comprises providing a cell that expresses an expression profile gene or fragments thereof. Preferred embodiments of the expression profile gene are genes which are differentially expressed in cancer cells, preferably colorectal cancer cells, compared to other cells. Preferred embodiments of expression profile genes used in the methods herein include but are not limited to the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9; fragments of the proteins of this group are also preferred. It is understood that molecules for use in the present invention may be from any figure or any subset of listed molecules. Therefore, for example, any one or more of the genes listed above can be used in the methods herein. In another embodiment, a nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided herein is a method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), the method comprising combining the CCMP and a candidate bioactive agent, and determining the binding of the candidate agent to the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein is a method for screening for a bioactive agent capable of modulating the activity of a CCMP. In one embodiment, the method comprises combining the CCMP and a candidate bioactive agent, and determining the effect of the candidate agent on the bioactivity of the CCMP. Preferably the CCMP is a protein or fragment thereof selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Also provided is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the CCMP, or an animal lacking the CCMP, for example as a result of a gene knockout.

Additionally, provided herein is a method of evaluating the effect of a candidate colorectal cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual.

Moreover, provided herein is a biochip comprising a nucleic acid segment which encodes a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably at least two nucleic acid segments are included. In another embodiment, the nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Furthermore, a method of diagnosing a disorder associated with colorectal cancer is provided. The method comprises determining the expression of a gene which encodes a colorectal cancer protein preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9 or a fragment thereof in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. A difference in the expression indicates that the first individual has a disorder associated with colorectal cancer.

In another aspect, the present invention provides an antibody which specifically binds to a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In a preferred embodiment, the fragment of CAA9 is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS. Other preferred fragments for the breast cancer proteins are shown in the figures. Preferably the antibody is a monoclonal antibody. The antibody can be a fragment of an antibody such as a single stranded antibody as further described herein, or can be conjugated to another molecule. In one embodiment, the antibody is a humanized antibody.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof. In a preferred embodiment, the method comprises combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof. The method further includes determining the binding of said CCMP or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the antibody as well as the agent inhibits colorectal cancer.

In a further aspect, a method for inhibiting colorectal cancer is provided. In one embodiment, the method comprises administering to a cell a composition comprising an antibody to a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment

thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. The method can be performed in vitro or in vivo, preferably in vivo to an individual. In a preferred embodiment the method of inhibiting colorectal cancer is provided to an individual with cancer. As described herein, methods of inhibiting colorectal cancer can be performed by administering an inhibitor of colorectal cancer protein activity, including antisense molecules, and preferably small molecules.

Also provided herein are methods eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a composition comprising a colorectal modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another aspect, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a colorectal cancer modulating protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, the nucleic acid is selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

A method of neutralizing the effect of a colorectal cancer protein, preferably selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7, CQA2, CGA8, CAA7 and CAA9, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from Figures 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14. Preferred nucleic acids are in Figure 12, more preferably Figure 13, and most preferably in Figure 14.

In another aspect of the invention, a method of treating an individual for colorectal cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of CJA8. In another embodiment, the method comprises administering to a patient having colorectal cancer an antibody to CJA8 conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radiolabeled isotope.

Also provided herein is a method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

Novel sequences are also provided herein. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

DETAILED DESCRIPTION OF THE FIGURES

Figure 1 provides the Accession numbers for genes, including expression sequence tags, (incorporated in their entirety here and throughout the application where Accession numbers are provided), upregulated in tumor tissue compared to normal colon tissue.

Figure 2 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 3 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 4 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Figure 5 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 6 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

- 5 Figure 7 provides the Accession numbers for genes, including expression sequence tags, downregulated in tumor tissue compared to normal colon tissue.

Figure 8 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- 10 Figure 9 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames in the sequences have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- Figure 10 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been
15 characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 11 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

- Figure 12 provides the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue. Open reading frames have been
20 characterized as having a signal sequence (SS), a transmembrane domain (TM) or other.

Figure 13 provides the Accession numbers for genes or fragments thereof, including descriptions of the gene or encoded protein, upregulated in tumor tissue compared to normal colon tissue.

- Figure 14 provides a list of proteins, including Accession numbers for nucleic acid sequences associated with the encoding genes thereof, upregulated in tumor tissue compared to normal colon
25 tissue.

Figure 15 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal protein provided herein, CAA2. The start and stop codon are shaded. The sequence within the two cross marks indicates a preferred novel fragment of CAA2 provided herein, referred to herein as the "CAA2 5' end". Preferred embodiments of CAA2 include at least a portion of the CAA2 5'. The sequence in bold and indicated with a bar at the bottom right beginning with "GGC" and ending with "AAA" can be found in Accession no. AA505133.

Figure 16 shows an embodiment of a nucleic acid encoding CAA2, wherein the start and stop codons are shaded.

Figure 17 shows an embodiment of an amino acid sequence of CAA2. Preferred fragments include at least about 10 amino acids in the N-terminal end. The N-terminus as defined herein includes an embodiment beginning at the first amino acid until about any one of the three amino acids marked with a dot above them. In another embodiment, the N-terminus of CAA2 is defined as the amino acid sequence encoded by the CAA2 5' end.

Figure 18 shows the amino acid sequence of CAA2p1, a preferred CAA2 fragment provided herein.

Figure 19 shows the amino acid sequence of CAA2p2, a preferred CAA2 fragment provided herein.

Figure 20 shows an alignment of the human and mouse CAA2 polypeptides provided herein. The mouse polypeptide contains at least some of the sequence of each of the following Accession numbers: AA386837; A1508773; AA505293; and AA636546.

Figure 21 shows the relative amount of expression of CAA2 in various samples of colon cancer tissue (dark bars) and many normal tissue types (light bars).

Figure 22 shows an embodiment of a colorectal cancer nucleic acid, CAA9 mRNA. The start and stop codons are underlined.

Figure 23 shows the open reading frame of the CAA9 gene wherein the start and stop codons are underlined.

Figure 24 shows an embodiment of the amino acid sequence of a colorectal cancer protein, CAA9, wherein putative transmembrane sequences are underlined. In one embodiment, CAA9 or fragments

of CAA9 are soluble, therefore, the transmembrane domains are deleted, inactivated, and/or the peptide is truncated (with or without re-ligation) to form soluble CAA9.

Figure 25 shows embodiments of colorectal cancer proteins (also termed colorectal cancer modulator proteins). Specifically, Figure 25 shows CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS and their respective solubilities.

Figure 26 shows the relative amount of CAA9 expression in several different samples of colon cancer tissue (dark bars) and normal tissues (light bars).

Figure 27 shows the nucleic acid sequence for the gene encoding CGA7. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA331393.

Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 28A and 28B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 29 shows the amino acid sequence of CGA7.

Figures 30A and 30B show the relative expression of CGA7 in normal tissue and colon cancer tissue, respectively.

Figure 31 shows the nucleic acid sequence for the mRNA encoding CGA8. Start (ATG) and stop (TAG) codons are indicated by shaded boxes. In bold is the sequence of Accession No. AA2786503. Underlined is the consensus sequence derived from the compilation and alignment of published est sequences.

Figures 32A and 32B show the alignment summary and descriptions, respectively, of the various est's (by accession number) compiled to generate the consensus sequence of figure 1.

Figure 33 shows the amino acid sequence of CGA8.

Figure 34 shows the relative expression of CGA8 in breast cancer tissue, colon cancer tissue, normal tissue and fetal tissue.

Figure 35 shows the sequence for the mRNA encoding CJA8. Start (ATG) and stop (TAA) codons are indicated by shaded boxes.

Figure 36 shows the amino acid sequence for CJA8. A putative transmembrane region is designated by shading. A mouse homolog of this human protein is found at Accession Number AAF21308.1.

- 5 Figure 37 shows the relative amount of expression of CJA8 in several different samples of colon tissues (dark bars) and normal tissues (light bars).

Figure 38 shows the relative amount of expression of BCN7 in several different samples of colon tissues (dark bars) and normal tissues (light bars), as determined using the sequence of Accession Number N22107 as a probe.

- 10 Figure 39 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, BCN7.

Figure 40 shows the sequence for the mRNA encoding CZA8. Start (ATG) and stop (TGA) codons are indicated by underlining.

- 15 Figure 41 shows the sequence for the mRNA encoding BCX2. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 42 shows the sequence for the mRNA encoding CBC2. Start (ATG) and stop (TAA) codons are indicated by underlining.

Figure 43 shows the sequence for the mRNA encoding CBC1. Start (ATG) and stop (TGA) codons are indicated by underlining.

- 20 Figure 44 shows the sequence for the mRNA encoding CBC3. Start (ATG) and stop (TGA) codons are indicated by underlining.

Figure 45 shows the sequence for the mRNA encoding BCN5. Start (ATG) and stop (TAA) codons are indicated by underlining.

- 25 Figure 46 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CJA9.

Figure 47 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA1.

Figure 48 shows an embodiment of a nucleic acid which includes a sequence which encodes a colorectal cancer protein provided herein, CQA2.

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DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel methods for diagnosis and prognosis evaluation for colorectal cancer (CRC), as well as methods for screening for compositions which modulate CRC. In one aspect, the expression levels of genes are determined in different patient samples for which either diagnosis or prognosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from CRC tissue, and within CRC tissue, different prognosis states (good or poor long term survival prospects, for example) may be determined. By comparing expression profiles of colon tissue in known different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are differentially expressed in CRC versus normal colon tissue, as well as differential expression resulting in different prognostic outcomes, allows the use of this information in a number of ways. For example, the evaluation of a particular treatment regime may be evaluated: does a chemotherapeutic drug act to improve the long-term prognosis in a particular patient. Similarly, diagnosis may be done or confirmed by comparing patient samples with the known expression profiles. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the CRC expression profile or convert a poor prognosis profile to a better prognosis profile. This may be done by making biochips comprising sets of the important CRC genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the CRC proteins can be evaluated for diagnostic and prognostic purposes or to screen candidate agents. In addition, the CRC nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the CRC proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in colorectal cancer, CRC, herein termed "CRC sequences". As outlined below, CRC sequences include those that are up-regulated (i.e. expressed at a higher level) in CRC, as well as those that are down-regulated (i.e. expressed at a lower level) in CRC. In a preferred embodiment, the CRC sequences are from humans; however, as will be appreciated by those in the art, CRC sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other CRC sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). CRC sequences from other organisms may be obtained using the techniques outlined below.

CRC sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the CRC sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid by polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a CRC protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form

not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the CRC sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, CRC sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the CRC sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, as outlined below, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate (Beaucage et al., *Tetrahedron* 49(10):1925 (1993) and references therein; Letsinger, *J. Org. Chem.* 35:3800 (1970); Sprinzl et al., *Eur. J. Biochem.* 81:579 (1977); Letsinger et al., *Nucl. Acids Res.* 14:3487 (1986); Sawai et al, *Chem. Lett.* 805 (1984), Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); and Pauwels et al., *Chemica Scripta* 26:141 (1986)), phosphorothioate (Mag et al., *Nucleic Acids Res.* 19:1437 (1991); and U.S. Patent No. 5,644,048), phosphorodithioate (Briu et al., *J. Am. Chem. Soc.* 111:2321 (1989), O-methylphosphoramidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press), and peptide nucleic acid backbones and linkages (see Egholm, *J. Am. Chem. Soc.* 114:1895 (1992); Meier et al., *Chem. Int. Ed. Engl.* 31:1008 (1992); Nielsen, *Nature*, 365:566 (1993); Carlsson et al., *Nature* 380:207 (1996), all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy et al., *Proc. Natl. Acad. Sci. USA* 92:6097 (1995); non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski et al., *Angew. Chem. Intl. Ed. English* 30:423 (1991); Letsinger et al., *J. Am. Chem. Soc.* 110:4470 (1988); Letsinger et al., *Nucleoside & Nucleotide* 13:1597 (1994); Chapters 2 and 3, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook; Mesmaeker et al., *Bioorganic & Medicinal Chem. Lett.* 4:395 (1994); Jeffs et al., *J. Biomolecular NMR* 34:17 (1994); *Tetrahedron Lett.* 37:743 (1996)) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, *ASC Symposium Series* 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins et al., *Chem. Soc. Rev.* (1995) pp169-176). Several nucleic acid analogs are described in Rawls, *C & E News* June 2, 1997 page 35. All of these references are hereby expressly incorporated by reference. These modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, all of these nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

5 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA
10 and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both
15 double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand ("Watson") also defines the sequence of the other strand ("Crick"); thus the sequences described herein also includes the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid contains any combination of deoxyribo- and ribo-nucleotides, and any combination of bases, including uracil, adenine, thymine,
20 cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

25 A CRC sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

30 The CRC sequences of the invention can be identified as follows. Samples of normal and tumor tissue are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are

commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated, and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the CRC screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, CRC sequences are those that are up-regulated in CRC; that is, the expression of these genes is higher in colorectal carcinoma as compared to normal colon tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. In addition, these genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In a preferred embodiment, CRC sequences are those that are down-regulated in CRC; that is, the expression of these genes is lower in colorectal carcinoma as compared to normal colon tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

CRC proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In a preferred embodiment the CRC protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, for example, signaling pathways); aberrant expression of such proteins results in unregulated or dysregulated cellular processes. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing intracellular proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In a preferred embodiment, the CRC sequences are transmembrane proteins. Transmembrane proteins are molecules that span the phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Important transmembrane protein receptors include, but are not limited to insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g. IL-1 receptor, IL-2 receptor, etc.

Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid

sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.

Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

CRC proteins that are transmembrane are particularly preferred in the present invention as they are good targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In a preferred embodiment, the CRC proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an

endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. CRC proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, for example for blood tests.

- 5 A CRC sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology to the CRC sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

- 10 As used herein, a nucleic acid is a "CRC nucleic acid" if the overall homology of the nucleic acid sequence to the nucleic acid sequences encoding the amino acid sequences of the figures is preferably greater than about 75%, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. Homology in this context means sequence similarity or identity, with identity being preferred. A preferred comparison for homology purposes is to compare
15 the sequence containing sequencing errors to the correct sequence. This homology will be determined using standard techniques known in the art, including, but not limited to, the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, PNAS USA 85:2444 (1988), by computerized implementations of these algorithms
20 (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, WI), the Best Fit sequence program described by Devereux et al., Nucl. Acid Res. 12:387-395 (1984), preferably using the default settings, or by inspection.

- In a preferred embodiment, the sequences which are used to determine sequence identity or similarity
25 are selected from the sequences set forth in the figures, preferably those represented in Figure 12, more preferably those represented in Figures 13A and 13B, still more preferably those of Figures 14-20, 22-25, 27-29, 31-33, 35-37 and 39-48, and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the
30 sequences are sequence variants as further described herein.

One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the

clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, J. Mol. Evol. 35:351-360 (1987); the method is similar to that described by Higgins & Sharp CABIOS 5:151-153 (1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in Altschul et al., J. Mol. Biol. 215, 403-410, (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul et al., Methods in Enzymology, 266: 460-480 (1996); <http://blast.wustl.edu/blast/REACRCE.html>. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of the sequences of the figures.

A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleosides than those of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences which encode the peptides identified in the figures, or their complements, are considered a CRC sequence. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al.,

both of which are hereby incorporated by reference. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g. 10 to 50 nucleotides) and at least about 60°C for long probes (e.g. greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, *supra*, and Tijssen, *supra*.

In addition, the CRC nucleic acid sequences of the invention are fragments of larger genes, i.e. they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, additional sequences of the CRC genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Maniatis et al., and Ausubel, et al., *supra*, hereby expressly incorporated by reference.

Once the CRC nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire CRC nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant CRC nucleic acid can be further-used as a probe to identify and isolate other CRC nucleic acids, for example additional coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant CRC nucleic acids and proteins.

The CRC nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the CRC nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene

therapy and/or antisense applications. Alternatively, the CRC nucleic acids that include coding regions of CRC proteins can be put into expression vectors for the expression of CRC proteins, again either for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to CRC nucleic acids (both the nucleic acid sequences encoding peptides outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the CRC nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of either electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent

binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant any material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic

acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as
5 alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, the oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

10 In an additional embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known
15 photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

In a preferred embodiment, CRC nucleic acids encoding CRC proteins are used to make a variety of expression vectors to express CRC proteins which can then be used in screening assays, as
20 described below. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the CRC protein. The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are
25 suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

30 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the

sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the CRC protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the CRC protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The CRC proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a CRC protein, under the appropriate conditions to

induce or cause expression of the CRC protein. The conditions appropriate for CRC protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melanogaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, THP1 cell line (a macrophage cell line) and human cells and cell lines.

In a preferred embodiment, the CRC proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral systems. A preferred expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, CRC proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the lac promoter is a hybrid of the *trp* and *lac* promoter sequences. Furthermore, a bacterial promoter can

include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the CRC protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, CRC proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, CRC protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The CRC protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the CRC protein may be fused to a carrier protein to form an immunogen. Alternatively, the CRC protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the CRC protein is a CRC peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In one embodiment, the CRC nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or

antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the CRC nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Accordingly, the present invention also provides CRC protein sequences. A CRC protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the CRC protein has homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The Input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of CRC proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques known in the art as are outlined above for the nucleic acid homologies.

CRC proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of CRC proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the CRC

nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the CRC proteins are derivative or variant CRC proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative CRC peptide will contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the CRC peptide.

Also included in an embodiment of CRC proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the CRC protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant CRC protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the CRC protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed CRC variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of CRC protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the

molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the CRC protein are desired, substitutions are generally made in accordance with the following chart:

Chart I
Exemplary Substitutions

5	Original Residue	
	Ala	Ser
	Arg	Lys
	Asn	Gln, His
	Asp	Glu
10	Cys	Ser
	Gln	Asn
	Glu	Asp
	Gly	Pro
	His	Asn, Gln
15	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	Met, Leu, Tyr
20	Ser	Thr
	Thr	Ser
	Trp	Tyr
	Tyr	Trp, Phe
	Val	Ile, Leu
25	Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the	
30	greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is	
35	substituted for (or by) one not having a side chain, e.g. glycine.	

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the CRC proteins as needed. Alternatively, the variant may be designed such that the biological activity of the CRC protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of CRC polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a CRC polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a CRC polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking CRC to a water-insoluble support matrix or surface for use in the method for purifying anti-CRC antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the CRC polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence CRC polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence CRC polypeptide.

Addition of glycosylation sites to CRC polypeptides may be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence CRC polypeptide (for O-linked glycosylation sites). The CRC amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the CRC polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the CRC polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the CRC polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of CRC comprises linking the CRC polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

CRC polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a CRC polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a CRC polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the CRC polypeptide. The presence of such epitope-tagged forms of a CRC polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the CRC polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a CRC polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

Also included with the definition of CRC protein in one embodiment are other CRC proteins of the CRC family, and CRC proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related CRC proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the CRC nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

In addition, as is outlined herein, CRC proteins can be made that are longer than those depicted in the figures, for example, by the elucidation of additional sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

CRC proteins may also be identified as being encoded by CRC nucleic acids. Thus, CRC proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the CRC protein is to be used to generate antibodies, for example for immunotherapy, the CRC protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller CRC protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from CAA2p1 and CAA2p2. In another preferred embodiment, the epitope is selected from CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA8p5 and CAA9p5MAPS.

In one embodiment, the term "antibody" includes antibody fragments, as are known in the art, including Fab, Fab₂, single chain antibodies (Fv for example), chimeric antibodies, etc., either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies.

Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the CAA2 or

fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 258:495 (1975).

In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include the CAA2 polypeptide or fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a CRC protein or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific.

In a preferred embodiment, the antibodies to CRC are capable of reducing or eliminating the biological function of CRC, as is described below. That is, the addition of anti-CRC antibodies (either polyclonal or preferably monoclonal) to CRC (or cells containing CRC) may reduce or eliminate the CRC activity.

Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the CRC proteins are humanized antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol.,

222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., BioTechnology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of CRC with an antibody raised against CRC proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active Immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen.

In a preferred embodiment the CRC proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted CRC protein.

In another preferred embodiment, the CRC protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the CRC protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane CRC protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the CRC protein. The antibody is also an antagonist of the CRC protein. Further, the antibody prevents activation of the transmembrane CRC protein. In one aspect, when the antibody prevents the binding of other molecules to the CRC protein, the antibody prevents growth of the cell. The antibody also sensitizes

the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity. Thus, CRC is treated by administering to a patient antibodies directed against the transmembrane CRC protein.

In another preferred embodiment, the antibody is conjugated to a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the CRC protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the CRC protein. The therapeutic moiety may inhibit enzymatic activity such as protease or protein kinase activity associated with CRC.

In a preferred embodiment, the therapeutic moiety may also be a cytotoxic agent. In this method, targeting the cytotoxic agent to tumor tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with CRC. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, croton, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against CRC proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane CRC proteins not only serves to increase the local concentration of therapeutic moiety in the CRC afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the CRC protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the CRC protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The CRC antibodies of the invention specifically bind to CRC proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^4 - 10^6 M^{-1} , with a preferred range being 10^7 - 10^9 M^{-1} .

In a preferred embodiment, the CRC protein is purified or isolated after expression. CRC proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the CRC protein may be purified using a standard anti-CRC antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the CRC protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the CRC proteins and nucleic acids are useful in a number of applications.

In one aspect, the expression levels of genes are determined for different cellular states in the CRC phenotype; that is, the expression levels of genes in normal colon tissue and in CRC tissue (and in some cases, for varying severities of CRC that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be done or confirmed: does tissue from a particular patient have the gene expression profile of normal or CRC tissue.

"Differential expression," or grammatical equivalents as used herein, refers to both qualitative as well as quantitative differences in the genes' temporal and/or cellular expression patterns within and among the cells. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, for example, normal versus CRC tissue. That is, genes may be turned on or turned off in a particular state, relative to another state. As is apparent to the skilled artisan, any comparison of two or more states can be made. Such a qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques in one such state or cell type, but is not detectable in both. Alternatively, the determination is quantitative in that expression is increased or decreased; that is, the expression of the gene is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard

characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e. upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably, at least about 200%, with from 300 to at least 1000% being especially preferred.

As will be appreciated by those in the art, this may be done by evaluation at either the gene transcript, or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Thus, the proteins corresponding to CRC genes, i.e. those identified as being important in a CRC phenotype, can be evaluated in a CRC diagnostic test.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well. Similarly, these assays may be done on an individual basis as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below in the example.

In a preferred embodiment nucleic acids encoding the CRC protein are detected. Although DNA or RNA encoding the CRC protein may be detected, of particular interest are methods wherein the mRNA encoding a CRC protein is detected. The presence of mRNA in a sample is an indication that the CRC gene has been transcribed to form the mRNA, and suggests that the protein is expressed. Probes to detect the mRNA can be any nucleotide/deoxynucleotide probe that is complementary to and base pairs with the mRNA and includes but is not limited to oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled

nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a CRC protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, any of the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in diagnostic assays. This can be done on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, CRC proteins, including intracellular, transmembrane or secreted proteins, find use as markers of CRC. Detection of these proteins in putative CRC tissue or patients allows for a determination or diagnosis of CRC. Numerous methods known to those of ordinary skill in the art find use in detecting CRC. In one embodiment, antibodies are used to detect CRC proteins. A preferred method separates proteins from a sample or patient by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be any other type of gel including isoelectric focusing gels and the like). Following separation of proteins, the CRC protein is detected by immunoblotting with antibodies raised against the CRC protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the CRC protein find use in *in situ* imaging techniques. In this method cells are contacted with from one to many antibodies to the CRC protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the CRC protein(s) contains a detectable label. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of CRC proteins. As will be appreciated by one of ordinary skill in the art, numerous other histological imaging techniques are useful in the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing CRC from blood samples. As previously described, certain CRC proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted CRC proteins. Antibodies can be used to detect the CRC by any of the previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like, as will be appreciated by one of ordinary skill in the art.

In a preferred embodiment, in situ hybridization of labeled CRC nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including CRC tissue and/or normal tissue, are made. In situ hybridization as is known in the art can then be done.

It is understood that when comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis as well as a prognosis. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to CRC severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, the CRC probes are attached to biochips for the detection and quantification of CRC sequences in a tissue or patient. The assays proceed as outlined for diagnosis.

In a preferred embodiment, any of the three classes of proteins as described herein are used in drug screening assays. The CRC proteins, antibodies, nucleic acids, modified proteins and cells containing CRC sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, Zlokarnik, et al., Science 279, 84-8 (1998), Heid, 1996 #69.

In a preferred embodiment, the CRC proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified CRC proteins are used in screening assays. That is, the present

invention provides novel methods for screening for compositions which modulate the CRC phenotype. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokam, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in CRC, candidate bioactive agents may be screened to modulate this gene's response; preferably to down regulate the gene, although in some circumstances to up regulate the gene. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tumor tissue, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4 fold increase in tumor compared to normal tissue, a decrease of about four fold is desired; a 10 fold decrease in tumor compared to normal tissue gives a 10 fold increase in expression for a candidate agent is desired.

As will be appreciated by those in the art, this may be done by evaluation at either the gene or the protein level; that is, the amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, for example through the use of antibodies to the CRC protein and standard immunoassays.

In a preferred embodiment, gene expression monitoring is done and a number of genes, i.e. an expression profile, is monitored simultaneously, although multiple protein expression monitoring can be done as well.

In this embodiment, the CRC nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of CRC sequences in a particular cell. The assays are further described below.

Generally, in a preferred embodiment, a candidate bioactive agent is added to the cells prior to analysis. Moreover, screens are provided to identify a candidate bioactive agent which modulates colorectal cancer, modulates CRC proteins, binds to a CRC protein, or interferes between the binding of a CRC protein and an antibody.

The term "candidate bioactive agent" or "drug candidate" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for bioactive agents that are capable of directly or indirectly altering either the CRC phenotype or the expression of a CRC sequence, including both nucleic acid sequences and protein sequences. In preferred embodiments, the bioactive agents modulate the expression profiles, or expression profile nucleic acids or proteins provided herein. In a particularly preferred embodiment, the candidate agent suppresses a CRC phenotype, for example to a normal colon tissue fingerprint. Similarly, the candidate agent preferably suppresses a severe CRC phenotype. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a candidate agent will neutralize the effect of a CRC protein. By "neutralize" is meant that activity of a protein is either inhibited or counter acted against so as to have substantially no effect on a cell.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random

chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

In a preferred embodiment, the candidate bioactive agents are proteins. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homo-phenylalanine, citrulline and noreucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chains may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradations.

In a preferred embodiment, the candidate bioactive agents are naturally occurring proteins or fragments of naturally occurring proteins. Thus, for example, cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of procaryotic and eucaryotic proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred.

In a preferred embodiment, the candidate bioactive agents are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a

defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

5 In a preferred embodiment, the candidate bioactive agents are nucleic acids, as defined above.

As described above generally for proteins, nucleic acid candidate bioactive agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

10 In a preferred embodiment, the candidate bioactive agents are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing the target sequences to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification
15 such as PCR occurring as needed, as will be appreciated by those in the art. For example, an in vitro transcription with labels covalently attached to the nucleosides is done. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target
20 sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin.
25 For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. As known in the art, unbound labeled streptavidin is removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can
30 comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670,

5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

5 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt
10 concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

15 The reactions outlined herein may be accomplished in a variety of ways, as will be appreciated by those in the art. Components of the reaction may be added simultaneously, or sequentially, in any order, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents may be included in the assays. These include reagents like salts, buffers, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Also reagents that otherwise
20 improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used, depending on the sample preparation methods and purity of the target.

Once the assay is run, the data is analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

25 The screens are done to identify drugs or bioactive agents that modulate the CRC phenotype. Specifically, there are several types of screens that can be run. A preferred embodiment is in the screening of candidate agents that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. That is, candidate agents that can mimic or produce an expression profile in CRC similar to the expression profile of normal colon tissue is expected to result in a suppression of the CRC phenotype. Thus, in this embodiment, mimicking an expression
30 profile, or changing one profile to another, is the goal.

In a preferred embodiment, as for the diagnosis and prognosis applications, having identified the differentially expressed genes important in any one state, screens can be run to alter the expression of the genes individually. That is, screening for modulation of regulation of expression of a single gene can be done; that is, rather than try to mimic all or part of an expression profile, screening for regulation of individual genes can be done. Thus, for example, particularly in the case of target genes whose presence or absence is unique between two states, screening is done for modulators of the target gene expression.

In a preferred embodiment, screening is done to alter the biological function of the expression product of the differentially expressed gene. Again, having identified the importance of a gene in a particular state, screening for agents that bind and/or modulate the biological activity of the gene product can be run as is more fully outlined below.

Thus, screening of candidate agents that modulate the CRC phenotype either at the gene expression level or the protein level can be done.

In addition screens can be done for novel genes that are induced in response to a candidate agent. After identifying a candidate agent based upon its ability to suppress a CRC expression pattern leading to a normal expression pattern, or modulate a single CRC gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated CRC tissue reveals genes that are not expressed in normal tissue or CRC tissue, but are expressed in agent treated tissue. These agent specific sequences can be identified and used by any of the methods described herein for CRC genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated CRC tissue sample.

Thus, in one embodiment, a candidate agent is administered to a population of CRC cells, that thus has an associated CRC expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e. a peptide) may be put into a viral construct such as a retroviral construct and added to the cell, such that expression of the peptide agent is accomplished; see PCT US97/01019, hereby expressly incorporated by reference.

Once the candidate agent has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, CRC tissue may be screened for agents that reduce or suppress the CRC phenotype. A change in at least one gene of the expression profile indicates that the agent has an effect on CRC activity. By defining such a signature for the CRC phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "CRC proteins" or a "CCMP". In preferred embodiments, the CCMP is as depicted in Figures 17-20, 24, 25, 29, 33 and 36, more preferably the protein having the sequence shown in Figures 29 or 36 or encoded by the sequences of Figures 27, 36 and 39-48. The CCMP may be a fragment, or alternatively, be the full length protein to a fragment shown herein. Preferably, the CCMP is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment.

In a preferred embodiment, the fragment is from CAA9. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the CAA9 fragment has an N-terminal Cys to aid in solubility. Preferably, the fragment is selected from CAA9p1, Caa9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.

In a preferred embodiment, the fragment is charged and from the c-terminus of CAA2. In one embodiment, the c-terminus of the fragment is kept as a free acid and the n-terminus is a free amine to aid in coupling, i.e., to cysteine. In another embodiment, the fragment is an internal peptide overlapping hydrophilic stretch of CAA2. In a preferred embodiment, the termini is blocked. Preferably, the fragment of CAA2 is selected from CAA2p1 or CAA2p2. In another preferred embodiment, the fragment is a novel fragment from the N-terminal. In one embodiment, the fragment excludes sequence outside of the N-terminal, in another embodiment, the fragment includes at least a portion of the N-terminal. "N-terminal" is used interchangeably herein with "N-terminus" which is further described above.

In one embodiment the CRC proteins are conjugated to an immunogenic agent as discussed herein.
In one embodiment the CRC protein is conjugated to BSA.

Thus, in a preferred embodiment, screening for modulators of expression of specific genes can be done. This will be done as outlined above, but in general the expression of only one or a few genes are evaluated.

In a preferred embodiment, screens are designed to first find candidate agents that can bind to differentially expressed proteins, and then these agents may be used in assays that evaluate the ability of the candidate agent to modulate differentially expressed activity. Thus, as will be appreciated by those in the art, there are a number of different assays which may be run; binding assays and activity assays.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. In general, this is done as is known in the art. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the CRC proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a CRC protein and a candidate bioactive agent, and determining the binding of the candidate agent to the CRC protein. Preferred embodiments utilize the human CRC protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative CRC proteins may be used.

Generally, in a preferred embodiment of the methods herein, the CRC protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the

composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the CRC protein is bound to the support, and a candidate bioactive agent is added to the assay. Alternatively, the candidate agent is bound to the support and the CRC protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the candidate bioactive agent to the CRC protein may be done in a number of ways. In a preferred embodiment, the candidate bioactive agent is labeled, and binding determined directly. For example, this may be done by attaching all or a portion of the CRC protein to a solid support, adding a labeled candidate agent (for example a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as is known in the art.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled. For example, the proteins (or proteinaceous candidate agents) may be labeled at tyrosine positions using ^{125}I , or with fluorophores. Alternatively, more than one component may be labeled with different labels; using ^{125}I for the proteins, for example, and a fluorophor for the candidate agents.

In a preferred embodiment, the binding of the candidate bioactive agent is determined through the use of competitive binding assays. In this embodiment, the competitor is a binding moiety known to bind to the target molecule (i.e. CRC), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding as between the bioactive agent and the binding moiety, with the binding moiety displacing the bioactive agent.

In one embodiment, the candidate bioactive agent is labeled. Either the candidate bioactive agent, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the candidate bioactive agent. Displacement of the competitor is an indication that the candidate bioactive agent is binding to the CRC protein and thus is capable of binding to, and potentially modulating, the activity of the CRC protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the candidate bioactive agent is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the candidate bioactive agent is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the bioactive agent is bound to the CRC protein with a higher affinity. Thus, if the candidate bioactive agent is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the candidate agent is capable of binding to the CRC protein.

In a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the activity of the CRC proteins. In this embodiment, the methods comprise combining a CRC protein and a competitor in a first sample. A second sample comprises a candidate bioactive agent, a CRC protein and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the CRC protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the CRC protein.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native CRC protein, but cannot bind to modified CRC proteins. The structure of the CRC protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect CRC bioactivity are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in any order that provides for the requisite binding.

Screening for agents that modulate the activity of CRC proteins may also be done. In a preferred embodiment, methods for screening for a bioactive agent capable of modulating the activity of CRC proteins comprise the steps of adding a candidate bioactive agent to a sample of CRC proteins, as above, and determining an alteration in the biological activity of CRC proteins. "Modulating the activity of CRC" includes an increase in activity, a decrease in activity, or a change in the type or kind of activity present. Thus, in this embodiment, the candidate agent should both bind to CRC proteins (although this may not be necessary), and alter its biological or biochemical activity as defined herein. The methods include both in vitro screening methods, as are generally outlined above, and in vivo screening of cells for alterations in the presence, distribution, activity or amount of CRC proteins.

Thus, in this embodiment, the methods comprise combining a CRC sample and a candidate bioactive agent, and evaluating the effect on CRC activity. By "CRC activity" or grammatical equivalents herein is meant one of the CRC's biological activities, including, but not limited to, cell division, preferably in colon tissue, cell proliferation, tumor growth, transformation of cells. In one embodiment, CRC activity includes activation of CZA8, BCX2, CBC2, CBC1, CBC3, CJA9, BCN5, CQA1, BCN7, CQA2, CJA8,

CAA2, CAA9, CGA7 and/or CGA8", preferably one of the CRC proteins listed in Figure 14. An inhibitor of CRC activity is the inhibition of any one or more CRC activities.

In a preferred embodiment, the activity of the CRC protein is increased; in another preferred embodiment, the activity of the CRC protein is decreased. Thus, bioactive agents that are antagonists are preferred in some embodiments, and bioactive agents that are agonists may be preferred in other embodiments.

In a preferred embodiment, the invention provides methods for screening for bioactive agents capable of modulating the activity of a CRC protein. The methods comprise adding a candidate bioactive agent, as defined above, to a cell comprising CRC proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a CRC protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, bioactive agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the CRC protein. In one embodiment, "colorectal cancer protein activity" as used herein includes at least one of the following: colorectal cancer activity, binding to CJA8, activation of CJA8 or activation of substrates of CJA8 by CJA8. In one embodiment, colorectal cancer activity is defined as the unregulated proliferation of colon tissue, or the growth of cancer in colon tissue. In one aspect, colorectal cancer activity as defined herein is related to the activity of CJA8 in the upregulation of CJA8 in colon cancer tissue.

In another embodiment, colorectal cancer protein activity includes at least one of the following: colorectal cancer activity, binding to one of CAA2, CAA9, CGA7 and CGA8, activation of one of CAA2, CAA9, CGA7, and CGA8 or activation of substrates of CAA2, CAA9, CGA7 or CGA8 by CAA2, CAA9, CGA7 or CGA8, respectively. In one preferred embodiment, CAA2 comprises its N-terminal end. In one aspect, colorectal cancer activity as defined herein is related to the activity of CAA2, CAA9, CGA7 and/or CGA8 in the upregulation of CAA2, CAA9, CGA7 and/or CGA8, respectively, in colon cancer tissue.

In one embodiment, a method of inhibiting colon cancer cell division is provided. The method comprises administration of a colorectal cancer inhibitor.

In another embodiment, a method of inhibiting tumor growth is provided. The method comprises administration of a colorectal cancer inhibitor.

- 5 In a further embodiment, methods of treating cells or individuals with cancer are provided. The method comprises administration of a colorectal cancer inhibitor.

In one embodiment, a colorectal cancer inhibitor is an antibody as discussed above. In another embodiment, the colorectal cancer inhibitor is an antisense molecule. Antisense molecules as used herein include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for colorectal cancer molecules. A preferred antisense molecule is for CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, BCN5, CQA1, BCN7, CQA2, CAA2, CAA9, CGA7 or CGA8, more preferably for the CRC sequences referenced in Figure 14, or for a ligand or activator thereof. A most preferred antisense molecule is for CJA8 or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

20 Antisense molecules may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

30 The compounds having the desired pharmacological activity may be administered in a physiologically acceptable carrier to a host, as previously described. The agents may be administered in a variety of

ways, orally, parenterally e.g., subcutaneously, intraperitoneally, intravascularly, etc. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt.%. The agents may be administered alone or in combination with other treatments, i.e., radiation.

5 The pharmaceutical compositions can be prepared in various forms, such as granules, tablets, pills, suppositories, capsules, suspensions, salves, lotions and the like. Pharmaceutical grade organic or inorganic carriers and/or diluents suitable for oral and topical use can be used to make up compositions containing the therapeutically-active compounds. Diluents known to the art include aqueous media, vegetable and animal oils and fats. Stabilizing agents, wetting and emulsifying
10 agents, salts for varying the osmotic pressure or buffers for securing an adequate pH value, and skin penetration enhancers can be used as auxiliary agents.

Without being bound by theory, it appears that the various CRC sequences are important in CRC. Accordingly, disorders based on mutant or variant CRC genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant CRC genes comprising determining all or part of the sequence of at least one endogenous CRC genes in a cell.
15 As will be appreciated by those in the art, this may be done using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the CRC genotype of an individual comprising determining all or part of the sequence of at least one CRC gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include
20 comparing the sequence of the sequenced CRC gene to a known CRC gene, i.e. a wild-type gene.

The sequence of all or part of the CRC gene can then be compared to the sequence of a known CRC gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the CRC gene of the patient and the known CRC gene is indicative of a disease state or a propensity for a disease state, as outlined herein.
25

In a preferred embodiment, the CRC genes are used as probes to determine the number of copies of the CRC gene in the genome.

In another preferred embodiment CRC genes are used as probed to determine the chromosomal localization of the CRC genes. Information such as chromosomal localization finds use in providing a
30

diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in CRC gene loci.

Thus, in one embodiment, methods of modulating CRC in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-CRC antibody that reduces or eliminates the biological activity of an endogenous CRC protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a CRC protein. As will be appreciated by those in the art, this may be accomplished in any number of ways. In a preferred embodiment, for example when the CRC sequence is down-regulated in CRC, the activity of the CRC gene is increased by increasing the amount of CRC in the cell, for example by overexpressing the endogenous CRC or by administering a gene encoding the CRC sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the erogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the CRC sequence is up-regulated in CRC, the activity of the endogenous CRC gene is decreased, for example by the administration of a CRC antisense nucleic acid.

In one embodiment, the CRC proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to CRC proteins, which are useful as described herein. Similarly, the CRC proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify CRC antibodies. In a preferred embodiment, the antibodies are generated to epitopes unique to a CRC protein; that is, the antibodies show little or no cross-reactivity to other proteins. These antibodies find use in a number of applications. For example, the CRC antibodies may be coupled to standard affinity chromatography columns and used to purify CRC proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the CRC protein.

In one embodiment, a therapeutically effective dose of a CRC or modulator thereof is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art, adjustments for CRC degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals, and organisms. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, and in the most preferred embodiment the patient is human.

5 The administration of the CRC proteins and modulators of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the CRC proteins and modulators may be directly applied as a solution or spray.

10 The pharmaceutical compositions of the present invention comprise a CRC protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or
15 otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable
20 base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines
25 and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

30 Additives are well known in the art, and are used in a variety of formulations.

In a preferred embodiment, CRC proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, CRC genes (including both the full-length

sequence, partial sequences, or regulatory sequences of the CRC coding regions) can be administered in gene therapy applications, as is known in the art. These CRC genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

- 5 In a preferred embodiment, CRC genes are administered as DNA vaccines, either single genes or combinations of CRC genes. Naked DNA vaccines are generally known in the art. Brower, Nature Biotechnology, 16:1304-1305 (1998).

- 10 In one embodiment, CRC genes of the present invention are used as DNA vaccines. Methods for the use of genes as DNA vaccines are well known to one of ordinary skill in the art, and include placing a CRC gene or portion of a CRC gene under the control of a promoter for expression in a CRC patient. The CRC gene used for DNA vaccines can encode full-length CRC proteins, but more preferably encodes portions of the CRC proteins including peptides derived from the CRC protein. In a preferred embodiment a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a CRC gene. Similarly, it is possible to immunize a patient with a plurality of
- 15 CRC genes or portions thereof as defined herein. Without being bound by theory, expression of the polypeptide encoded by the DNA vaccine, cytotoxic T-cells, helper T-cells and antibodies are induced which recognize and destroy or eliminate cells expressing CRC proteins.

- In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the CRC polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are known to those of ordinary skill in the art and find use in the invention.
- 20

- In another preferred embodiment CRC genes find use in generating animal models of CRC. As is appreciated by one of ordinary skill in the art, when the CRC gene identified is repressed or diminished in CRC tissue, gene therapy technology wherein antisense RNA directed to the CRC gene will also diminish or repress expression of the gene. An animal generated as such serves as an animal model of CRC that finds use in screening bioactive drug candidates. Similarly, gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence of the CRC protein. When desired, tissue-specific expression or knockout of the CRC protein may be necessary.
- 25

- 30 It is also possible that the CRC protein is overexpressed in CRC. As such, transgenic animals can be generated that overexpress the CRC protein. Depending on the desired expression level, promoters

of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of CRC and are additionally useful in screening for bioactive molecules to treat CRC.

- 5 It is understood that the examples described herein in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references and sequences of accession numbers cited herein are incorporated by reference in their entirety.

EXAMPLES

Example 1

10 Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

- Estimate tissue weight. Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. Use the 20mm generator for tissue weighing more than 0.6g. If the working volume is greater than 2ml, then homogenize tissue in a 15ml polypropylene tube (Falcon 2059). Fill tube no greater than 10ml.
- 15

HOMOGENIZATION

- Before using generator, it should have been cleaned after last usage by running it through soapy H₂O and rinsing thoroughly. Run through with EtOH to sterilize. Keep tissue frozen until ready. Add TRIzol directly to frozen tissue then homogenize.
- 20

- Following homogenization, remove insoluble material from the homogenate by centrifugation at 7500 x g for 15 min. in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. Transfer the cleared homogenate to a new tube(s). The samples may be frozen now at -60 to -70°C (and kept for at least one month) or you may continue with the purification.
- 25

PHASE SEPARATION

Incubate the homogenized samples for 5 minutes at room temperature.
Add 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization.
Cap tubes securely and shake tubes vigorously by hand (do not vortex) for 15 seconds.

Incubate samples at room temp. for 2-3 minutes. Centrifuge samples at 6500rpm in a Sorvall superspeed for 30 min. at 4°C. (You may spin at up to 12,000 x g for 10 min. but you risk breaking your tubes in the centrifuge.)

RNA PRECIPITATION

- 5 Transfer the aqueous phase to a fresh tube. Save the organic phase if isolation of DNA or protein is desired. Add 0.5ml of Isopropyl alcohol per 1ml of TRIzol reagent used in the original homogenization. Cap tubes securely and invert to mix. Incubate samples at room temp. for 10 minutes. Centrifuge samples at 6500rpm in Sorvall for 20min. at 4°C.

RNA WASH

- 10 Pour off the supernate. Wash pellet with cold 75% ethanol. Use 1ml of 75% ethanol per 1ml of TRIzol reagent used in the initial homogenization. Cap tubes securely and invert several times to loosen pellet. (Do not vortex). Centrifuge at <8000rpm (<7500 x g) for 5 minutes at 4°C. Pour off the wash. Carefully transfer pellet to an eppendorf tube (let it slide down the tube into the new tube and use a pipet tip to help guide it in if necessary). Depending on the volumes you are working with, you can decide what size tube(s) you want to precipitate the RNA in. When I tried leaving the RNA in the large 15ml tube, it took so long to dry (i.e. it did not dry) that I eventually had to transfer it to a smaller tube. Let pellet dry in hood. Resuspend RNA in an appropriate volume of DEPC H₂O. Try for 2-5ug/ul. Take absorbance readings.
- 15

Purify poly A+ mRNA from total RNA or clean up total RNA with Qiagen's

RNeasy kit

- 20 Purification of poly A+ mRNA from total RNA. Heat oligotex suspension to 37°C and mix immediately before adding to RNA. Incubate Elution Buffer at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature.
- 25

Centrifuge for 2 minutes at 14,000 to 18,000 g. If centrifuge has a "soft setting," then use it. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Save sup until certain that satisfactory binding and elution of poly A+ mRNA has occurred.

- 30 Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed (soft setting if possible) for 1 minute.

Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein.

Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low.

Read absorbance, using diluted Elution Buffer as the blank.

Before proceeding with cDNA synthesis, the mRNA must be precipitated. Some component leftover or in the Elution Buffer from the Oligotex purification procedure will inhibit downstream enzymatic reactions of the mRNA.

10 Ethanol Precipitation

Add 0.4 vol. of 7.5 M NH₄OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Dry the last bit of ethanol from the pellet in the hood.

15 (Do not speed vacuum). Suspend pellet in DEPC H₂O at 1ug/ul concentration.

Clean up total RNA using Qiagen's RNeasy kit

Add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. If concerned about yield, re-apply flowthrough to column and centrifuge again.

20 Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube and apply 30-50ul of RNase-free

25 water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. Take absorbance reading. If necessary, ethanol precipitate with ammonium acetate and 2.5X volume 100% ethanol.

Make cDNA using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

First Strand cDNA Synthesis

- Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

Second Strand Synthesis

Place 1st strand reactions on ice.

- Add: 91ul DEPC H₂O
 10 30ul 5X 2nd Strand Buffer
 3ul 10mM dNTP mix
 1ul 10U/ul *E.coli* DNA Ligase
 4ul 10U/ul *E.coli* DNA Polymerase
 15 1ul 2U/ul RNase H

Make the above into a mix if there are more than 2 samples. Mix and incubate 2 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA

Clean up cDNA

Phenol:Chloroform:Isoamyl Alcohol (25:24:1) purification using Phase-Lock gel tubes:

- 20 Centrifuge PLG tubes for 30 sec at maximum speed. Transfer cDNA mix to PLG tube. Add equal volume of phenol:chloroform:isoamyl alcohol and shake vigorously (do not vortex). Centrifuge 5 minutes at maximum speed. Transfer top aqueous solution to a new tube. Ethanol precipitate: add 7.5X 5M NH₄OAc and 2.5X volume of 100% ethanol. Centrifuge immediately at room temp. for 20 min, maximum speed. Remove sup then wash pellet 2X with cold 80% ethanol. Remove
 25 as much ethanol wash as possible then let pellet air dry. Resuspend pellet in 3ul RNase-free water.

In vitro Transcription (IVT) and labeling with biotin

Pipet 1.5ul of cDNA into a thin-wall PCR tube.

Make NTP labeling mix:

- 30 Combine at room temperature: 2ul T7 10xATP (75mM) (Ambion)
 2ul T7 10xGTP (75mM) (Ambion)
 1.5ul T7 10xCTP (75mM) (Ambion)

- Enzo)
- 5
- | | |
|--------|-----------------------------------------------|
| 1.5ul | T7 10xUTP (75mM) (Ambion) |
| 3.75ul | 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or |
| 3.75ul | 10mM Bio-16-CTP (Enzo) |
| 2ul | 10x T7 transcription buffer (Ambion) |
| 2ul | 10x T7 enzyme mix (Ambion) |

Final volume of total reaction is 20ul. Incubate 6 hours at 37C in a PCR machine.

RNeasy clean-up of IVT product

Follow previous instructions for RNeasy columns or refer to Qiagen's RNeasy protocol handbook.

- 10 cRNA will most likely need to be ethanol precipitated. Resuspend in a volume compatible with the fragmentation step.

Fragmentation

- 15 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer.

5 x Fragmentation buffer:

- 200 mM Tris-acetate, pH 8.1
- 500 mM KOAc
- 20 150 mM MgOAc

The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

Hybridization

- 25 200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made.

Hybridization Mix: fragment labeled RNA (50ng/ul final conc.)

50 pM 948-b control oligo

1.5 pM BioB

5 pM BioC

25 pM BioD

100 pM CRE

0.1mg/ml herring sperm DNA

0.5mg/ml acetylated BSA

to 300 ul with 1xMES hyb. buffer

The instruction manuals for the products used herein are incorporated herein in their entirety.

Labelling Protocol Provided Herein

Hybridization reaction:

Start with non-biotinylated IVT (purified by RNeasy columns)

(see example 1 for steps from tissue to IVT)

IVT antisense RNA; 4 µg: µl

Random Hexamers (1 µg/µl): 4 µl

H₂O: µl

14 µl

- Incubate 70°C, 10 min. Put on ice.

Reverse transcription:

5X First Strand (BRL) buffer: 6 µl

0.1 M DTT: 3 µl

50X dNTP mix: 0.6 µl

H₂O: 2.4 µl

Cy3 or Cy5 dUTP (1mM): 3 µl

SS RT II (BRL): 1 µl

16 µl

- Add to hybridization reaction.

- Incubate 30 min., 42°C.

- Add 1 µl SSII and let go for another hour.

Put on ice.

- 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 μ l each of 100mM dATP, dCTP, and dGTP; 10 μ l of 100mM dTTP to 15 μ l H₂O. dNTPs from Pharmacia)

RNA degradation:

5

86 μ l H₂O

- Add 1.5 μ l 1M NaOH/ 2mM EDTA, incubate at 65°C, 10 min.

10 μ l 10N NaOH

4 μ l 50mM EDTA

U-Con 30

500 µl TE/sample spin at 7000g for 10 min, save flow through for purification

10

Qiagen purification:

- suspend u-con recovered material in 500ul buffer PB

-proceed w/ normal Qiagen protocol

DNAse digest:

- Add 1 μ l of 1/100 dil of DNase/30 μ l Rx and incubate at 37°C for 15 min.

15

-5 min 95°C to denature enzyme

Sample preparation:

- Add:

Cot-1 DNA: 10 μ l

50X dNTPs: 1 μ l

20

20X SSC: 2.3 μ l

Na pyro phosphate: 7.5 μ l

10mg/ml Herring sperm DNA 1ul of 1/10 dilution

21.8 final vol.

- Dry down in speed vac.

25

- Resuspend in 15 μ l H₂O.

- Add 0.38 μ l 10% SDS.

- Heat 95°C, 2 min.

- Slow cool at room temp. for 20 min.

Put on slide and hybridize overnight at 64°C.

30

Washing after the hybridization:

3X SSC/0.03% SDS;

2 min. 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H₂O

1X SSC; 5 min.

12.5 mls 20X SSC in 250mls H₂O

0.2X SSC: 5 min. 2.5 mls 20X SSC in 250mls H₂O

Dry slides in centrifuge, 1000 RPM, 1min.

Scan at appropriate PMT's and channels.

The results are shown in Figures 1 through 11. The lists of genes come from colorectal tumors from a variety of stages of the disease. The genes that are up regulated in the tumors (overall) were also found to be expressed at a limited amount or not at all in the body map. The body map for the colorectal project consists of ten tissues: Heart, Brain, Lung, Liver, Breast, Kidney, Prostate, Small Intestine, Spleen, and Colon. The down regulated genes in tumors (overall) versus normal colon were not selected for their expression or lack of expression in the body map. As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length. Figure 1 shows 51 upregulated genes; Figure 2 shows 194 upregulated genes; Figure 3 shows 1144 upregulated genes and Figure 4 shows 1815 upregulated genes. The genes shown in Figures 1 and 5 are particularly preferred. Figure 5 shows 54 downregulated genes; Figure 6 shows 558 downregulated genes; and Figure 7 shows 1923 downregulated genes; and Figures 8, 9, 10 and 11 provide the Accession numbers for genes, including expression sequence tags, upregulated in tumor tissue compared to normal colon tissue.

Example 2

Expression studies were performed herein.

As indicated in Figure 21, CAA2 is upregulated in colon cancer tissue. CAA2 is found in chromosome 15, cytoband 15q15-22, interval D15S146-D15S117. CAA2 has N-myristoylation sites and a C-terminal microbody targeting signal. The preferred fragments shown in Figures 18 and 19 have a solubility of 1 mg/ 1 ml H₂O.

As indicated in Figure 26, CAA9 is upregulated in colon cancer tissue. CAA9 is found in chromosome 5, cytoband 5q23.3, interval D5S471-D5S393.

As indicated in Figures 30A and 30B, CGA7 is upregulated in colon cancer tissue. CGA7 is found in chromosome 2.

As indicated in Figure 34, CGA8 is upregulated in colon cancer tissue.

As indicated in Figure 37, CJA8 is upregulated in colon cancer tissue. CJA8 is found in chromosome 11.

As indicated in Figure 38, BCN7 is upregulated in colon cancer tissue. BCN7 is found in chromosome 5, cytoband 5q22, interval D5S471-D5S393.

CLAIMS

We claim:

1. A method of screening drug candidates comprising:
 - a) providing a cell that expresses an expression profile gene which encodes a protein selected from the group consisting of CZA8, BCX2, CBC2, CBC1, CBC3, CJA8, CJA9, CGA7, BCN5, CQA1, BCN7 and CQA2 or a fragment thereof;
 - b) adding a drug candidate to said cell; and
 - c) determining the effect of said drug candidate on the expression of said expression profile gene.
2. A method according to claim 1 wherein said determining comprises comparing the level of expression in the absence of said drug candidate to the level of expression in the presence of said drug candidate, wherein the concentration of said drug candidate can vary when present, and wherein said comparison can occur after addition or removal of the drug candidate.
3. A method according to claim 1 wherein the expression of said profile gene is decreased as a result of the introduction of the drug candidate.
4. A method of screening for a bioactive agent capable of binding to a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the binding of said candidate agent to said CCMP.
5. A method for screening for a bioactive agent capable of modulating the activity of a colorectal cancer modulator protein (CCMP), wherein said CCMP is CJA8 or a fragment thereof, said method comprising combining said CCMP and a candidate bioactive agent, and determining the effect of said candidate agent on the bioactivity of said CCMP.
6. A method of evaluating the effect of a candidate colorectal cancer drug comprising:
 - a) administering said drug to a patient;
 - b) removing a cell sample from said patient; and
 - c) determining the expression profile of said cell.
7. A method according to claim 6 further comprising comparing said expression profile to an expression profile of a healthy individual.

8. A biochip comprising a nucleic acid segment encoding CJA81 or a fragment thereof, wherein said biochip comprises fewer than 1000 nucleic acid probes.
9. A method of diagnosing colorectal cancer comprising:
- 5 a) determining the expression of a gene encoding CJA8 or a fragment thereof in a first tissue type of a first individual; and
- b) comparing said expression of said gene from a second normal tissue type from said first individual or a second unaffected individual;
- wherein a difference in said expression indicates that the first individual has colorectal cancer.
10. An antibody which specifically binds to CJA8, or a fragment thereof.
- 10 11. An antibody which specifically binds to CAA9, or a fragment thereof.
12. The antibody of Claim 11 wherein said fragment is selected from the group CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 and CAA9p5MAPS.
13. The antibody of Claim 10, wherein said antibody is a monoclonal antibody.
14. The antibody of Claim 10, wherein said antibody is a humanized antibody.
- 15 15. The antibody of Claim 10, wherein said antibody is an antibody fragment.
16. A method for screening for a bioactive agent capable of interfering with the binding of a colorectal cancer modulator protein (CCMP) or a fragment thereof and an antibody which binds to said CCMP or fragment thereof, said method comprising:
- 20 a) combining a CCMP or fragment thereof, a candidate bioactive agent and an antibody which binds to said CCMP or fragment thereof; and
- b) determining the binding of said CCMP or fragment thereof and said antibody.
17. A method for inhibiting colorectal cancer, said method comprising administering to a cell a composition comprising an antibody to CAJ8 or a fragment thereof.
18. The method of Claim 17 wherein said cell is a cell of an individual.
- 25 19. The method of Claim 18 wherein said individual has cancer.

20. The method of Claim 17 wherein said antibody is a humanized antibody.
21. The method of Claim 17 wherein said antibody is an antibody fragment.
22. A method for inhibiting colorectal cancer in a cell, wherein said method comprises administering to a cell a composition comprising antisense molecules to CJA8.
- 5 23. A peptide consisting essentially of CAA9p1, CAA9p2, CAA9p3, CAA9p4, CAA9p4MAPS, CAA9p5 or CAA9p5MAPS.
24. A composition comprising the peptide of Claim 23.
25. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising CJA8 or a fragment thereof.
- 10 26. A method of eliciting an immune response in an individual, said method comprising administering to said individual a composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof.
27. A composition capable of eliciting an immune response in an individual, said composition comprising CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
- 15 28. A composition capable of eliciting an immune response in an individual, said composition comprising a nucleic acid comprising a sequence encoding CJA8 or a fragment thereof and a pharmaceutically acceptable carrier.
29. A method of treating an individual for colorectal cancer comprising administering to said individual an inhibitor of CJA8.
- 20 30. The method of Claim 29 wherein said inhibitor is an antibody.
31. A method for determining the prognosis of an individual with colorectal cancer comprising determining the level of CJA8 in a sample, wherein a high level of CJA8 indicates a poor prognosis.

32. A method of neutralizing the effect of a CJA8, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization.

5 33. A method for localizing a therapeutic moiety to colorectal cancer tissue comprising exposing said tissue to an antibody to CJA8 or fragment thereof conjugated to said therapeutic moiety.

34. The method of Claim 33, wherein said therapeutic moiety is a cytotoxic agent.

35. The method of Claim 33, wherein said therapeutic moiety is a radioisotope.

10 36. A method of treating colorectal cancer comprising administering to an individual having colorectal cancer an antibody to CJA8 or fragment thereof conjugated to a therapeutic moiety.

37. The method of Claim 36, wherein said therapeutic moiety is a cytotoxic agent.

38. The method of Claim 36, wherein said therapeutic moiety is a radioisotope.

FIGURE 1

Primary Key	fold upregulated in tumor over normal colon	Accession	Unigene Cluster	Unigene Descriptor
37677	>10	AA460530	HS 96384	Homo sapiens orphan G protein-coupled receptor HG38 mRNA complete cds
4479	>10	X69886	HS 32036	H.sapiens mRNA for NBK apoptotic inducer protein
6148	>10	U30246	HS 110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
18330	>10	AA216722	HS 54481	Human mRNA for apolipoprotein E receptor 2 complete cds
5592	>10	X17644	HS 2707	G1 to S phase transition 1
16610	>10	AA035336	HS 128949	PBK1
33109	>10	W99961	HS 22564	Human mRNA for KIAA0393 gene complete cds
37246	>10	AA449311	HS 98658	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds
2857	>10	M85937	HS 2173	Fucosyltransferase 4 (alpha (13) fucosyltransferase myeloid-specific)
14338	>10	AA598712	HS 23723	ESTs Weakly similar to ORF YP1212c [S cerevisiae]
4676	9.6	U55206	HS 76619	Homo sapiens human gamma-glutamyl hydrolase (HGH) mRNA complete cds
2192	7.6	L43211	HS 20954	Homo sapiens angiotensin II receptor gene complete cds
5793	7.4	X54942	HS 63758	CDC28 protein kinase 2
18231	6.3	AA199747	HS 79025	Human mRNA for KIAA0096 gene partial cds
6051	6.1	X68314	HS 2704	Glutathione peroxidase 2 gastrointestinal
27117	5.0	AA05098	HS 36178	ESTs Weakly similar to MOESIN/VEZIN/RADIXIN HOMOLOG [D.melanogaster]
12669	5.0	AA417030	HS 5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HG3961-HT3127	EST - HG3961-HT3127	
2157	4.6	L41939	HS 89403	Homo sapiens protein-tyrosine kinase EPHE2v (EPHB2) mRNA complete cds
13193	4.4	AA442763	HS 20463	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]
5690	4.4	X17620	HS 118638	NUCLEOSIDE DIPHOSPHATE KINASE A
28050	4.1	AA479139	HS 75393	Acid phosphatase 1 soluble
4540	3.5	U48807	HS 2359	Human MAP kinase phosphatase (MKP-2) mRNA complete cds
26105	3.1	AA243133	HS 46915	Homo sapiens serine/threonine kinase (BTA1K) mRNA complete cds
19177	3.1	H10984	HS 12338	ESTs
5780	3.1	X54448	HS 789	GRO1 oncogene (melanoma growth stimulating activity alpha)
33620	3.0	W93943	HS 59509	ESTs
4536	2.9	U48705	HS 75562	Receptor protein-tyrosine kinase EDDR1
5928	2.9	X62046	HS 75166	WEE1-LIKE PROTEIN KINASE
28258	2.8	AA050133	HS 62273	ESTs
21256	2.7	R09186	HS 151355	Homo sapiens mRNA for KIAA0054 protein partial cds

FIGURE 1 (CONT.)

27748	2.5	A4453159	Hs 41723	Human kinase-like spindle protein HKSP (HKSP) mRNA complete cds
28510	2.5	AA046745	Hs.110457	ESTs
28640	2.4	M30448	EST - M30448	
3834	2.3	U12595	Hs.2204	Human tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA partial cds
4674	2.3	U54959	Hs.93121	Human LGN protein mRNA complete cds
5769	2.3	X53800	Hs.69590	GRO3 oncogene
25050	2.3	A4011134	Hs.25863	ESTs Weakly similar to rein [H.sapiens]
41935	2.3	T25651	Hs.75761	Human serine kinase mRNA complete cds
26895	2.3	A232765	Hs.42550	H.sapiens mRNA for M-phase phosphoprotein mpp5
1782	2.1	L12711	Hs.69543	Transketolase (Wernicke-Korsakoff syndrome)
25993	2.1	AA113749	Hs.8730	Homo sapiens IPL (IPL) mRNA complete cds
1487	1.8	J03934	Hs.80706	NAD(P)H-menaioone oxidoreductase
7656	1.5	AA203428	Hs.7756	ESTs Moderately similar to ANKYRIN BRAIN VARIANT 2 [Homo sapiens]
683	1.5	D79957	Hs.41697	Human mRNA for KIAA0175 gene complete cds
636	1.5	D67444	Hs.75305	Human mRNA for KIAA0255 gene complete cds
3088	1.2	M77836	Hs.79217	PYRROLINE-5-CARBOXYLATE REDUCTASE
6879	1.1	Z28066	Hs.60896	H.sapiens nek2 mRNA for protein kinase
6880	1.0	Z28067	Hs.2235	H.sapiens nek3 mRNA for protein kinase
2473	0.7	M21504	Hs.79748	Antigen identified by monoclonal antibodies 4f2 TRA1:10 TROP4 and T43
36508	0.7	AA425921	Hs.75063	Human 100 kDa coactivator mRNA complete cds

FIGURE 2

Primary Key	Field Suppressed of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
33616	>10	W83726	Hs.55279	Protease inhibitor 5 (maspin)
34197	>10	A4232315	Hs.12540	Homo sapiens clone 23797 and 23917 mRNA partial cds
19387	>10	H20128	Hs.31656	ESTs
8125	>10	A4330771	Hs.82911	Human protein-tyrosine phosphatase (HLPP-1) mRNA partial sequence
18362	>10	A4223912	Hs.12013	Ribonuclease L (2'-5'-oligopuridine synthetase-dependent) inhibitor
39995	>10	H62474	Hs.108240	EST
19328	>10	H17608	Hs.22858	ESTs
38590	>10	A4398648	Hs.78202	Human mRNA for transcriptional activator HSNF2b complete cds
38456	>10	A4504343	Hs.101074	ESTs
17559	>10	AA128407	Hs.71190	ESTs
5819	>10	X14850	Hs.2711	HISTONE H2A.X
4029	>10	U27080	Hs.74598	Human DNA polymerase delta small subunit mRNA complete cds
15006	>10	U30246	Hs.110736	Human tumetidine-sensitive Na ⁺ -K ⁺ -Cl cotransporter (NKCC1) mRNA complete cds
3859	>10	U04313	Hs.55279	Protease inhibitor 5 (maspin)
28916	>10	A4331393	Hs.47378	ESTs
1346	>10	HG4716-HT5158	EST - HG4716-HT5158	
37491	10.0	AA455239	Hs.87630	ESTs Highly similar to CHROMOSOME CONDENSATION PROTEIN DPY-27 [Caenorhabditis elegans]
13110	9.8	AA435940	Hs.19114	Homo sapiens mRNA for high mobility group protein HMGB3
4676	8.8	U55206	Hs.78819	Homo sapiens human gamma-glutamyl hydrolase (IGH) mRNA complete cds
21655	8.7	R38239	Hs.25276	EST
14723	8.3	D58694	Hs.34782	ESTs
5783	7.4	X54942	Hs.83758	GDC28 protein kinase 2
29848	7.1	N22107	Hs.124215	ESTs
9347	7.0	H03686	Hs.112013	ESTs
6078	7.0	X89141	Hs.48876	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE
9326	6.8	D89377	Mth (Microspora)	homeo box homolog 2
1556	8.7	J05614	Hs.89404	EST - J05614
25675	8.7	AA129757	Hs.54902	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]
20126	8.4	N20215	Hs.19457	ESTs
6061	8.1	X88314	Hs.2704	Glutathione peroxidase 2 gastrin-induced
10667	6.1	AA088458	Hs.19322	ESTs Weakly similar to KLU SUBFAMILY 1
19062	6.0	AA179845	Hs.73825	ESTs Moderately similar to radkinease-6 [Mus musculus]
4093	5.9	U25182	Hs.83383	Human antioxidant enzyme AOE37.2 mRNA complete cds
15230	5.8	AA211901	Hs.85430	ESTs
5330	5.8	U91327	EST - U91327	
4244	5.7	U33286	Hs.90073	Human chromosome segregation gene homolog CAS mRNA complete cds

FIGURE 2 (CONT.)

6928	5.7	Z46029	Hs.2315	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)
6160	5.6	X74794	Hs.39699	CD221 HOMOLOG
31487	5.4	N69507	Hs.129849	ESTs
9470	5.3	H46617	EST - H46617	
33458	5.0	W66535	Hs.14158	Homo sapiens mRNA for KIAA0636 protein complete cds
12659	5.0	AA417030	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds
1106	4.8	HG2881-HT3127	EST - HG2881-HT3127	
34397	4.8	AA251758	Hs.40323	Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA complete cds
11595	4.8	AA242819	Hs.32539	ESTs
17622	4.8	AA421594	Hs.71435	ESTs Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]
34754	4.7	AA287642	Hs.81848	Human mRNA for KIAA0078 gene complete cds
25038	4.7	AA010065	Hs.83758	CD28 protein kinase 2
5312	4.6	U80716	Hs.79187	Human cell surface protein HCAR mRNA complete cds
8085	4.6	AA314779	Hs.105484	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
8264	4.5	AA401334	Hs.50542	ESTs
34479	4.5	AA252080	Hs.106941	ESTs
7885	4.4	AA053319	Hs.110736	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds
10716	4.4	X17620	Hs.81634	ESTs
5690	4.4	X17620	Hs.9951	ESTs
20203	4.3	N26855	Hs.118638	NUCLEOSIDE DIPHOSPHATE KINASE A
10923	4.2	AA116036	Hs.6958	ESTs Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
28050	4.1	AA479139	Hs.9329	ESTs
10970	4.1	AA126380	Hs.75393	Acid phosphatase 1 soluble
4149	4.1	U28386	Hs.5285	ESTs
5767	4.1	X33783	Hs.2397	RAG (recombination activating gene) cohort 1
26596	4.0	AA275943	Hs.118226	MULTIFUNCTIONAL PROTEIN ADE2
8961	3.9	AFFX-	Hs.88671	ESTs
38604	3.9	AA398803	Hs.111496	AFFX-HUMFROM1507_3
30560	3.9	N49284	Hs.1334	MYB PROTO-ONCOGENE PROTEIN
8513	3.8	AA446960	Hs.103135	ESTs
14509	3.8	AA005943	Hs.32783	ESTs
25284	3.8	AA045074	Hs.110146	ESTs Weakly similar to 52-KD SS-Autoantigen [H.sapiens]
27354	3.8	AA425221	Hs.81688	ESTs
18385	3.8	AA422719	Hs.110826	Homo sapiens CAGF9 mRNA partial cds
25240	3.7	AA039713	Hs.110406	ESTs
16854	3.7	U07550	Hs.71622	ESTs Weakly similar to KIAA0319 [H.sapiens]
3709	3.7	AA456437	Hs.1197	Heat shock 10 KD protein 1 (chaperonin 10)
13606	3.5		Hs.20386	ESTs Weakly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]
8338	3.4	AA117152	Hs.5101	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds

FIGURE 2 (CONT.)

387	D26569	EST - D26569	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]
16843	W59247	Hs.27437	ESTs
13838	AA465342	Hs.34045	ESTs
251	D14520	Hs.84728	Basic transcription element binding protein 2
3778	U08848	Hs.363	Zinc finger protein 139 (clone pH2-37)
5680	Hs16396	Hs.37791	NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE
17365	AA101551	Hs.68900	ESTs
33965	AA181580	Hs.81690	Homo sapiens importin beta subunit mRNA complete cds
19233	H12534	Hs.8104	ESTs
13767	AA463224	Hs.119387	ESTs
4738	U68766	Hs.75801	Human FX protein mRNA complete cds
17041	AA070364	EST - RC_AA070364	ESTs
15504	W28362	Hs.44131	Human translation initiation factor eIF3 p66 subunit mRNA complete cds
7401	AA024600	Hs.55682	ESTs Highly similar to INORGANIC PYROPHOSPHATASE [Bos taurus]
16883	F04258	Hs.30454	ESTs Weakly similar to IIII ALU SUBFAMILY [H.sapiens]
23930	T96930	Hs.125123	ESTs
11288	AA118512	Hs.25916	Thymidylate synthase
170	D00596	Hs.82962	ESTs
11859	AA251503	Hs.36708	Homo sapiens MAD3-like protein kinase mRNA complete cds
14134	AA49080	Hs.33668	ESTs Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]
11140	AA158132	Hs.11817	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]
17925	AA164209	Hs.31730	Homo sapiens RRM RNA binding protein Goy-tp (GRY-RBP) mRNA complete cds
26630	AA278650	Hs.73291	ESTs
7445	AA110423	Hs.110048	ESTs
18055	AA179387	Hs.73596	ESTs
15174	U82967	Hs.87246	Human Rcl-2 binding component 3 (buc3) mRNA, partial cds
33620	W69343	Hs.59509	ESTs
1932	L24804	Hs.75639	Human (b23) mRNA complete cds
39566	F03738	Hs.3657	ESTs
1605	L00058	Hs.79070	V-myc avian myeloblastosis viral oncogene homolog
4538	U48705	Hs.75552	Receptor protein-tyrosine kinase EDDR1
36200	AA421164	Hs.107213	ESTs
12313	AA397816	Hs.22595	ESTs
19867	H61476	Hs.15641	ESTs
6081	X65398	Hs.82685	CD47 antigen (Rb-related antigen integrin-associated signal transducer)
16708	AA043944	Hs.62063	ESTs
357	D26156	Hs.78022	Human mRNA for transcriptional activator tSNF2b complete cds
8059	AA310967	Hs.5080	ESTs Weakly similar to T04A6.11 [C.elegans]
35830	AA411448	Hs.135386	ESTs
20151	N20895	Hs.6831	Homo sapiens clone 1400 unknown protein mRNA, partial cds

FIGURE 2 (CONT.)

17352	2.3	AA100925	ESTs	Hs.20680	EST - RC_D51272_s
28796	2.3	D51272	ESTs	Hs.4310	ESTs
28679	2.3	AA287133	Hs.4611	Human sapiens protein tyrosine phosphatase PTP1B mRNA complete cds	ESTs
24092	2.3	W42845	Hs.35352	Membrane cofactor protein (CD46 trophoblast-lymphocyte cross-reactive antigen)	ESTs
5975	2.3	X59405	Hs.7391	Human sapiens voltage dependent anion channel protein mRNA complete cds	ESTs
7404	2.3	AA094989	Hs.7391	H sapiens mRNA for Sm protein G	ESTs
6388	2.3	X85733	Hs.74366	ESTs Weakly similar to renin [H.sapiens]	ESTs
25050	2.3	AA011134	Hs.25863	Human serine kinase mRNA complete cds	ESTs
41955	2.3	T28881	Hs.75761	Human serine kinase mRNA complete cds	ESTs
3343	2.3	M57336	Hs.21486	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	ESTs
5937	2.2	X52534	Hs.50684	High-mobility group (nonhistone chromosomal) protein 2	ESTs
7387	2.2	AA050977	Hs.71475	ESTs	ESTs
20943	2.2	N69552	Hs.5663	Human sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	ESTs
28448	2.2	AA627552	Hs.76887	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	EST - D79129
651	2.2	D78129	Hs.103300	Human sapiens diaphanin protein-2 (DPH2) mRNA complete cds	ESTs
11688	2.2	AA256772	Hs.21214	ESTs	ESTs
11803	2.2	AA257971	Hs.1334	MYB PROTO-ONCOGENE PROTEIN	ESTs
4046	2.2	U23376	Hs.27931	ESTs	ESTs
20276	2.2	N32919	Hs.194568	ESTs Weakly similar to HYPOTHETICAL 37.4 KO PROTEIN IN MER2-CPY2 INTERGENIC REGION [Saccharomyces cerevisiae]	ESTs
34370	2.1	AA251829	Hs.10600	ESTs Weakly similar to HYPOTHETICAL 39.6 KO PROTEIN IN MTD1-NUP133 INTERGENIC REGION [Saccharomyces cerevisiae]	EST - S75256
14582	2.1	AA621340	EST - S75256	EST - HG1112-HT112	EST - S75256
3461	2.1	S75256	Hs.77899	Tropomyosin alpha chain (skeletal muscle)	ESTs
924	2.1	HG1112-HT112	Hs.15313	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE BRR2 [S.cerevisiae]	ESTs
24348	2.1	W86469	Hs.18770	Isochaque-RNA synthetase	ESTs
10898	2.1	AA112053	Hs.10724	ESTs Weakly similar to unknown [S.cerevisiae]	ESTs
381	2.1	D28473	Hs.8130	Human sapiens IPL (IPL) mRNA complete cds	ESTs
11528	2.1	AA236018	Hs.107213	ESTs	ESTs
25553	2.1	AA113149	Hs.83550	Human heterochromatin protein HP-H gamma mRNA complete cds	ESTs
38040	2.1	AA481403	Hs.83379	Cytochrome c oxidase subunit Vb	ESTs
411	2.1	U26312	Hs.88668	Cytochrome c oxidase subunit Vb	EST - D33423
611	2.0	AC020115	Hs.83379	Cytochrome c oxidase subunit Vb	EST - D33423
9112	2.0	D16611	Hs.83379	Cytochrome c oxidase subunit Vb	EST - D33423
390	2.0	D28403	Hs.42582	ESTs	ESTs
377	2.0	D28364	Hs.5920	ESTs	ESTs
28379	2.0	AA609710	Hs.9654	Human gene 121711 defective mariner transposon Hmar2 mRNA sequence	ESTs
24230	2.0	W72276	Hs.104558	ESTs	ESTs
40212	2.0	H85635			
8118	2.0	AA328693			

FIGURE 3 (CONT.)

30647	15	N06648	Hs 42093	EST	
35106	15	AA37146.1	Hs 142555	EST	Weakly similar to putative p152 (H-seg)
35190	15	N03884	Hs 44403	EST	
4286	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
11014	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
4157	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
30770	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
30656	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
4479	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
37051	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
34604	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
31134	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
3013	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
40604	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
21238	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
2657	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
10608	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
33300	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
34155	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
35039	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
8723	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
32115	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
20088	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
25265	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
33713	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
15892	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
42860	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
35000	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
20500	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
27068	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
41700	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
30729	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
42807	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
31872	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
32404	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)
3375	15	N03884	Hs 44403	EST	Weakly similar to putative p152 (H-seg)

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FIGURE 3 (CONT.)

42290	15	719135	EST	Hs 1428175	EST	Y19564	15	719135	EST	Hs 1428175	EST	Y19564
4419	15	X01648	EST	Hs 13117	EST	Y19564	15	X01648	EST	Hs 13117	EST	Y19564
3337	15	C03719	EST	Hs 15436	EST	Y19564	15	C03719	EST	Hs 15436	EST	Y19564
3319	15	N13465	EST	Hs 15173	EST	Y19564	15	N13465	EST	Hs 15173	EST	Y19564
29116	15	A025276	EST	Hs 15067	EST	Y19564	15	A025276	EST	Hs 15067	EST	Y19564
4113	15	H09203	EST	Hs 15060	EST	Y19564	15	H09203	EST	Hs 15060	EST	Y19564
19501	15	A025276	EST	Hs 15060	EST	Y19564	15	A025276	EST	Hs 15060	EST	Y19564
354	15	A025276	EST	Hs 15060	EST	Y19564	15	A025276	EST	Hs 15060	EST	Y19564
33900	15	A025276	EST	Hs 15060	EST	Y19564	15	A025276	EST	Hs 15060	EST	Y19564
26603	15	A025276	EST	Hs 15060	EST	Y19564	15	A025276	EST	Hs 15060	EST	Y19564
26635	15	A025276	EST	Hs 15060	EST	Y19564	15	A025276	EST	Hs 15060	EST	Y19564
15115	15	A025276	EST	Hs 15060	EST	Y19564	15	A025276	EST	Hs 15060	EST	Y19564
30112	15	T05715	EST	Hs 17960	EST	Y19564	15	T05715	EST	Hs 17960	EST	Y19564
31512	15	T05715	EST	Hs 17960	EST	Y19564	15	T05715	EST	Hs 17960	EST	Y19564
31512	15	T05715	EST	Hs 17960	EST	Y19564	15	T05715	EST	Hs 17960	EST	Y19564
11903	15	A010334	EST	Hs 11024	EST	Y19564	15	A010334	EST	Hs 11024	EST	Y19564
4071	15	L05206	EST	Hs 10200	EST	Y19564	15	L05206	EST	Hs 10200	EST	Y19564
34462	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
30906	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
4507	15	L05206	EST	Hs 10200	EST	Y19564	15	L05206	EST	Hs 10200	EST	Y19564
4970	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
11920	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
11708	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
40541	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
29643	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
11987	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
12865	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
30528	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
15088	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
40112	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
22874	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
4507	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
32196	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
15059	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
41907	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
3346	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564
7175	15	A021587	EST	Hs 10200	EST	Y19564	15	A021587	EST	Hs 10200	EST	Y19564

FIGURE 3 (CONT.)

3	7	R001843	EST: RC_A039043	
3	7	R01812	EST: RC_A35026	EST: RC_A35026
3	7	R01813	EST: RC_A35027	EST: RC_A35027
3	7	R01814	EST: RC_A35028	EST: RC_A35028
3	7	R01815	EST: RC_A35029	EST: RC_A35029
3	7	R01816	EST: RC_A35030	EST: RC_A35030
3	7	R01817	EST: RC_A35031	EST: RC_A35031
3	7	R01818	EST: RC_A35032	EST: RC_A35032
3	7	R01819	EST: RC_A35033	EST: RC_A35033
3	7	R01820	EST: RC_A35034	EST: RC_A35034
3	7	R01821	EST: RC_A35035	EST: RC_A35035
3	7	R01822	EST: RC_A35036	EST: RC_A35036
3	7	R01823	EST: RC_A35037	EST: RC_A35037
3	7	R01824	EST: RC_A35038	EST: RC_A35038
3	7	R01825	EST: RC_A35039	EST: RC_A35039
3	7	R01826	EST: RC_A35040	EST: RC_A35040
3	7	R01827	EST: RC_A35041	EST: RC_A35041
3	7	R01828	EST: RC_A35042	EST: RC_A35042
3	7	R01829	EST: RC_A35043	EST: RC_A35043
3	7	R01830	EST: RC_A35044	EST: RC_A35044
3	7	R01831	EST: RC_A35045	EST: RC_A35045
3	7	R01832	EST: RC_A35046	EST: RC_A35046
3	7	R01833	EST: RC_A35047	EST: RC_A35047
3	7	R01834	EST: RC_A35048	EST: RC_A35048
3	7	R01835	EST: RC_A35049	EST: RC_A35049
3	7	R01836	EST: RC_A35050	EST: RC_A35050
3	7	R01837	EST: RC_A35051	EST: RC_A35051
3	7	R01838	EST: RC_A35052	EST: RC_A35052
3	7	R01839	EST: RC_A35053	EST: RC_A35053
3	7	R01840	EST: RC_A35054	EST: RC_A35054
3	7	R01841	EST: RC_A35055	EST: RC_A35055
3	7	R01842	EST: RC_A35056	EST: RC_A35056
3	7	R01843	EST: RC_A35057	EST: RC_A35057
3	7	R01844	EST: RC_A35058	EST: RC_A35058
3	7	R01845	EST: RC_A35059	EST: RC_A35059
3	7	R01846	EST: RC_A35060	EST: RC_A35060
3	7	R01847	EST: RC_A35061	EST: RC_A35061
3	7	R01848	EST: RC_A35062	EST: RC_A35062
3	7	R01849	EST: RC_A35063	EST: RC_A35063
3	7	R01850	EST: RC_A35064	EST: RC_A35064
3	7	R01851	EST: RC_A35065	EST: RC_A35065
3	7	R01852	EST: RC_A35066	EST: RC_A35066
3	7	R01853	EST: RC_A35067	EST: RC_A35067
3	7	R01854	EST: RC_A35068	EST: RC_A35068
3	7	R01855	EST: RC_A35069	EST: RC_A35069
3	7	R01856	EST: RC_A35070	EST: RC_A35070
3	7	R01857	EST: RC_A35071	EST: RC_A35071
3	7	R01858	EST: RC_A35072	EST: RC_A35072
3	7	R01859	EST: RC_A35073	EST: RC_A35073
3	7	R01860	EST: RC_A35074	EST: RC_A35074
3	7	R01861	EST: RC_A35075	EST: RC_A35075
3	7	R01862	EST: RC_A35076	EST: RC_A35076
3	7	R01863	EST: RC_A35077	EST: RC_A35077
3	7	R01864	EST: RC_A35078	EST: RC_A35078
3	7	R01865	EST: RC_A35079	EST: RC_A35079
3	7	R01866	EST: RC_A35080	EST: RC_A35080
3	7	R01867	EST: RC_A35081	EST: RC_A35081
3	7	R01868	EST: RC_A35082	EST: RC_A35082
3	7	R01869	EST: RC_A35083	EST: RC_A35083
3	7	R01870	EST: RC_A35084	EST: RC_A35084
3	7	R01871	EST: RC_A35085	EST: RC_A35085
3	7	R01872	EST: RC_A35086	EST: RC_A35086
3	7	R01873	EST: RC_A35087	EST: RC_A35087
3	7	R01874	EST: RC_A35088	EST: RC_A35088
3	7	R01875	EST: RC_A35089	EST: RC_A35089
3	7	R01876	EST: RC_A35090	EST: RC_A35090
3	7	R01877	EST: RC_A35091	EST: RC_A35091
3	7	R01878	EST: RC_A35092	EST: RC_A35092
3	7	R01879	EST: RC_A35093	EST: RC_A35093
3	7	R01880	EST: RC_A35094	EST: RC_A35094
3	7	R01881	EST: RC_A35095	EST: RC_A35095
3	7	R01882	EST: RC_A35096	EST: RC_A35096
3	7	R01883	EST: RC_A35097	EST: RC_A35097
3	7	R01884	EST: RC_A35098	EST: RC_A35098
3	7	R01885	EST: RC_A35099	EST: RC_A35099
3	7	R01886	EST: RC_A35100	EST: RC_A35100
3	7	R01887	EST: RC_A35101	EST: RC_A35101
3	7	R01888	EST: RC_A35102	EST: RC_A35102
3	7	R01889	EST: RC_A35103	EST: RC_A35103
3	7	R01890	EST: RC_A35104	EST: RC_A35104
3	7	R01891	EST: RC_A35105	EST: RC_A35105
3	7	R01892	EST: RC_A35106	EST: RC_A35106
3	7	R01893	EST: RC_A35107	EST: RC_A35107
3	7	R01894	EST: RC_A35108	EST: RC_A35108
3	7	R01895	EST: RC_A35109	EST: RC_A35109
3	7	R01896	EST: RC_A35110	EST: RC_A35110
3	7	R01897	EST: RC_A35111	EST: RC_A35111
3	7	R01898	EST: RC_A35112	EST: RC_A35112
3	7	R01899	EST: RC_A35113	EST: RC_A35113
3	7	R01900	EST: RC_A35114	EST: RC_A35114
3	7	R01901	EST: RC_A35115	EST: RC_A35115
3	7	R01902	EST: RC_A35116	EST: RC_A35116
3	7	R01903	EST: RC_A35117	EST: RC_A35117
3	7	R01904	EST: RC_A35118	EST: RC_A35118
3	7	R01905	EST: RC_A35119	EST: RC_A35119
3	7	R01906	EST: RC_A35120	EST: RC_A35120
3	7	R01907	EST: RC_A35121	EST: RC_A35121
3	7	R01908	EST: RC_A35122	EST: RC_A35122
3	7	R01909	EST: RC_A35123	EST: RC_A35123
3	7	R01910	EST: RC_A35124	EST: RC_A35124
3	7	R01911	EST: RC_A35125	EST: RC_A35125
3	7	R01912	EST: RC_A35126	EST: RC_A35126
3	7	R01913	EST: RC_A35127	EST: RC_A35127
3	7	R01914	EST: RC_A35128	EST: RC_A35128
3	7	R01915	EST: RC_A35129	EST: RC_A35129
3	7	R01916	EST: RC_A35130	EST: RC_A35130
3	7	R01917	EST: RC_A35131	EST: RC_A35131
3	7	R01918	EST: RC_A35132	EST: RC_A35132
3	7	R01919	EST: RC_A35133	EST: RC_A35133
3	7	R01920	EST: RC_A35134	EST: RC_A35134
3	7	R01921	EST: RC_A35135	EST: RC_A35135
3	7	R01922	EST: RC_A35136	EST: RC_A35136
3	7	R01923	EST: RC_A35137	EST: RC_A35137
3	7	R01924	EST: RC_A35138	EST: RC_A35138
3	7	R01925	EST: RC_A35139	EST: RC_A35139
3	7	R01926	EST: RC_A35140	EST: RC_A35140
3	7	R01927	EST: RC_A35141	EST: RC_A35141
3	7	R01928	EST: RC_A35142	EST: RC_A35142
3	7	R01929	EST: RC_A35143	EST: RC_A35143
3	7	R01930	EST: RC_A35144	EST: RC_A35144
3	7	R01931	EST: RC_A35145	EST: RC_A35145
3	7	R01932	EST: RC_A35146	EST: RC_A35146
3	7	R01933	EST: RC_A35147	EST: RC_A35147
3	7	R01934	EST: RC_A35148	EST: RC_A35148
3	7	R01935	EST: RC_A35149	EST: RC_A35149
3	7	R01936	EST: RC_A35150	EST: RC_A35150
3	7	R01937	EST: RC_A35151	EST: RC_A35151
3	7	R01938	EST: RC_A35152	EST: RC_A35152
3	7	R01939	EST: RC_A35153	EST: RC_A35153
3	7	R01940	EST: RC_A35154	EST: RC_A35154
3	7	R01941	EST: RC_A35155	EST: RC_A35155
3	7	R01942	EST: RC_A35156	EST: RC_A35156
3	7	R01943	EST: RC_A35157	EST: RC_A35157
3	7	R01944	EST: RC_A35158	EST: RC_A35158
3	7	R01945	EST: RC_A35159	EST: RC_A35159
3	7	R01946	EST: RC_A35160	EST: RC_A35160
3	7	R01947	EST: RC_A35161	EST: RC_A35161
3	7	R01948	EST: RC_A35162	EST: RC_A35162
3	7	R01949	EST: RC_A35163	EST: RC_A35163
3	7	R01950	EST: RC_A35164	EST: RC_A35164
3	7	R01951	EST: RC_A35165	EST: RC_A35165
3	7	R01952	EST: RC_A35166	EST: RC_A35166
3	7	R01953	EST: RC_A35167	EST: RC_A35167
3	7	R01954	EST: RC_A35168	EST: RC_A35168
3	7	R01955	EST: RC_A35169	EST: RC_A35169
3	7	R01956	EST: RC_A35170	EST: RC_A35170
3	7	R01957	EST: RC_A35171	EST: RC_A35171
3	7	R01958	EST: RC_A35172	EST: RC_A35172
3	7	R01959	EST: RC_A35173	EST: RC_A35173
3	7	R01960	EST: RC_A35174	EST: RC_A35174
3	7	R01961	EST: RC_A35175	EST: RC_A35175
3	7	R01962	EST: RC_A35176	EST: RC_A35176
3	7	R01963	EST: RC_A35177	EST: RC_A35177
3	7	R01964	EST: RC_A35178	EST: RC_A35178
3	7	R01965	EST: RC_A35179	EST: RC_A35179
3	7	R01966	EST: RC_A35180	EST: RC_A35180
3	7	R01967	EST: RC_A35181	EST: RC_A35181
3	7	R01968	EST: RC_A35182	EST: RC_A35182
3	7	R01969	EST: RC_A35183	EST: RC_A35183
3	7	R01970	EST: RC_A35184	EST: RC_A35184
3	7	R01971	EST: RC_A35185	EST: RC_A35185
3	7	R01972	EST: RC_A35186	EST: RC_A35186
3	7	R01973	EST: RC_A35187	EST: RC_A35187
3	7	R01974	EST: RC_A35188	EST: RC_A35188
3	7	R01975	EST: RC_A35189	EST: RC_A35189
3	7	R01976	EST: RC_A35190	EST: RC_A35190
3	7	R01977	EST: RC_A35191	EST: RC_A35191
3	7	R01978	EST: RC_A35192	EST: RC_A35192
3	7	R01979	EST: RC_A35193	EST: RC_A35193
3	7	R01980	EST: RC_A35194	EST: RC_A35194
3	7	R01981	EST: RC_A35195	EST: RC_A35195
3	7	R01982	EST: RC_A35196	EST: RC_A35196
3	7	R01983	EST: RC_A35197	EST: RC_A35197
3	7	R01984	EST: RC_A35198	EST: RC_A35198
3	7	R01985	EST: RC_A35199	EST: RC_A35199
3	7	R01986	EST: RC_A35200	EST: RC_A35200
3	7	R01987	EST: RC_A35201	EST: RC_A35201
3	7	R01988	EST: RC_A35202	EST: RC_A35202
3	7	R01989	EST: RC_A35203	EST: RC_A35203
3	7	R01990	EST: RC_A35204	EST: RC_A35204
3	7	R01991	EST: RC_A35205	EST: RC_A35205
3	7	R01992	EST: RC_A35206	EST: RC_A35206
3	7	R01993	EST: RC_A35207	EST: RC_A35207
3	7	R01994	EST: RC_A35208	EST: RC_A35208
3	7	R01995	EST: RC_A35209	EST: RC_A35209
3	7	R01996	EST: RC_A35210	EST: RC_A35210
3	7	R01997	EST: RC_A35211	EST: RC_A35211
3	7	R01998	EST: RC_A35212	EST: RC_A35212
3	7	R01999	EST: RC_A35213	EST: RC_A35213
3	7	R02000	EST: RC_A35214	EST: RC_A35214
3	7	R02001	EST: RC_A35215	EST: RC_A35215
3	7	R02002	EST: RC_A35216	EST: RC_A35216
3	7	R02003	EST: RC_A35217	EST: RC_A35217
3	7	R02004	EST: RC_A35218	EST: RC_A35218
3	7	R02005	EST: RC_A35219	EST: RC_A35219
3	7	R02006	EST: RC_A35220	EST: RC_A35220
3	7	R02007	EST: RC_A35221	EST: RC_A35221
3	7	R02008	EST: RC_A35222	EST: RC_A35222
3	7	R02009	EST: RC_A35223	EST: RC_A35223
3	7	R02010	EST: RC_A35224	EST: RC_A35224
3	7	R02011	EST: RC_A35225	EST: RC_A35225
3	7	R02012	EST: RC_A35226	EST: RC_A35226
3	7	R02013	EST: RC_A35227	EST: RC_A35227
3	7	R02014	EST: RC_A35228	EST: RC_A35228
3	7	R02015	EST: RC_A35229	EST: RC_A35229
3	7	R02016	EST: RC_A35230	EST: RC_A35230
3	7	R02017	EST: RC_A35231	EST: RC_A35231
3	7	R02018	EST: RC_A35232	EST: RC_A35232
3	7	R02019	EST: RC_A35233	EST: RC_A35233
3	7	R02020	EST: RC_A35234	EST: RC_A35234
3	7	R02021	EST: RC_A35235	EST: RC_A35235
3	7	R02022	EST: RC_A35236	EST: RC_A35236
3	7	R02023	EST: RC_A35237	EST: RC_A35237
3	7	R02024	EST: RC_A35238	EST: RC_A35238
3	7	R02025	EST: RC_A35239	EST: RC_A35239
3	7	R02026	EST: RC_A35240	EST: RC_A35240
3	7	R02027	EST: RC_A35241	EST: RC_A35241
3	7	R02028	EST: RC_A35242	EST: RC_A35242
3	7	R02029	EST: RC_A35243	EST: RC_A35243
3	7	R02030	EST: RC_A35244	EST: RC_A35244
3	7	R02031	EST: RC_A35245	EST: RC_A35245
3	7	R02032	EST: RC_A35246	EST: RC_A35246
3	7	R02033	EST: RC_A35247	EST: RC_A35247
3	7	R02034	EST: RC_A35248	EST: RC_A35248
3	7	R02035	EST: RC_A35249	EST: RC_A35249
3	7	R02036	EST: RC_A35250	EST: RC_A35250
3	7	R02037	EST: RC_A35251	EST: RC_A35251
3	7	R02038	EST: RC_A35252	EST: RC_A35252
3	7	R02039	EST: RC_A35253	EST: RC_A35253
3	7	R02040		

FIGURE 3 (CONT.)

190500	13	H025509	Hs 74039	EST*
200500	33	AA278550	Hs 72951	EST*
210500	33	Hs 72951	Hs 72951	EST*
220500	33	Hs 72951	Hs 72951	EST*
230500	33	Hs 72951	Hs 72951	EST*
240500	33	Hs 72951	Hs 72951	EST*
250500	33	Hs 72951	Hs 72951	EST*
260500	33	Hs 72951	Hs 72951	EST*
270500	33	Hs 72951	Hs 72951	EST*
280500	33	Hs 72951	Hs 72951	EST*
290500	33	Hs 72951	Hs 72951	EST*
300500	33	Hs 72951	Hs 72951	EST*
310500	33	Hs 72951	Hs 72951	EST*
320500	33	Hs 72951	Hs 72951	EST*
330500	33	Hs 72951	Hs 72951	EST*
340500	33	Hs 72951	Hs 72951	EST*
350500	33	Hs 72951	Hs 72951	EST*
360500	33	Hs 72951	Hs 72951	EST*
370500	33	Hs 72951	Hs 72951	EST*
380500	33	Hs 72951	Hs 72951	EST*
390500	33	Hs 72951	Hs 72951	EST*
400500	33	Hs 72951	Hs 72951	EST*
410500	33	Hs 72951	Hs 72951	EST*
420500	33	Hs 72951	Hs 72951	EST*
430500	33	Hs 72951	Hs 72951	EST*
440500	33	Hs 72951	Hs 72951	EST*
450500	33	Hs 72951	Hs 72951	EST*
460500	33	Hs 72951	Hs 72951	EST*
470500	33	Hs 72951	Hs 72951	EST*
480500	33	Hs 72951	Hs 72951	EST*
490500	33	Hs 72951	Hs 72951	EST*
500500	33	Hs 72951	Hs 72951	EST*
510500	33	Hs 72951	Hs 72951	EST*
520500	33	Hs 72951	Hs 72951	EST*
530500	33	Hs 72951	Hs 72951	EST*
540500	33	Hs 72951	Hs 72951	EST*
550500	33	Hs 72951	Hs 72951	EST*
560500	33	Hs 72951	Hs 72951	EST*
570500	33	Hs 72951	Hs 72951	EST*
580500	33	Hs 72951	Hs 72951	EST*
590500	33	Hs 72951	Hs 72951	EST*
600500	33	Hs 72951	Hs 72951	EST*
610500	33	Hs 72951	Hs 72951	EST*
620500	33	Hs 72951	Hs 72951	EST*
630500	33	Hs 72951	Hs 72951	EST*
640500	33	Hs 72951	Hs 72951	EST*
650500	33	Hs 72951	Hs 72951	EST*
660500	33	Hs 72951	Hs 72951	EST*
670500	33	Hs 72951	Hs 72951	EST*
680500	33	Hs 72951	Hs 72951	EST*
690500	33	Hs 72951	Hs 72951	EST*
700500	33	Hs 72951	Hs 72951	EST*
710500	33	Hs 72951	Hs 72951	EST*
720500	33	Hs 72951	Hs 72951	EST*
730500	33	Hs 72951	Hs 72951	EST*
740500	33	Hs 72951	Hs 72951	EST*
750500	33	Hs 72951	Hs 72951	EST*
760500	33	Hs 72951	Hs 72951	EST*
770500	33	Hs 72951	Hs 72951	EST*
780500	33	Hs 72951	Hs 72951	EST*
790500	33	Hs 72951	Hs 72951	EST*
800500	33	Hs 72951	Hs 72951	EST*
810500	33	Hs 72951	Hs 72951	EST*
820500	33	Hs 72951	Hs 72951	EST*
830500	33	Hs 72951	Hs 72951	EST*
840500	33	Hs 72951	Hs 72951	EST*
850500	33	Hs 72951	Hs 72951	EST*
860500	33	Hs 72951	Hs 72951	EST*
870500	33	Hs 72951	Hs 72951	EST*
880500	33	Hs 72951	Hs 72951	EST*
890500	33	Hs 72951	Hs 72951	EST*
900500	33	Hs 72951	Hs 72951	EST*
910500	33	Hs 72951	Hs 72951	EST*
920500	33	Hs 72951	Hs 72951	EST*
930500	33	Hs 72951	Hs 72951	EST*
940500	33	Hs 72951	Hs 72951	EST*
950500	33	Hs 72951	Hs 72951	EST*
960500	33	Hs 72951	Hs 72951	EST*
970500	33	Hs 72951	Hs 72951	EST*
980500	33	Hs 72951	Hs 72951	EST*
990500	33	Hs 72951	Hs 72951	EST*
1000500	33	Hs 72951	Hs 72951	EST*

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FIGURE 3 (CONT.)

2	HA147	HA1203	ET4
3	HA18021	HA1604	ET4
4	HA18021	HA1604	ET4
5	HA18021	HA1604	ET4
6	HA18021	HA1604	ET4
7	HA18021	HA1604	ET4
8	HA18021	HA1604	ET4
9	HA18021	HA1604	ET4
10	HA18021	HA1604	ET4
11	HA18021	HA1604	ET4
12	HA18021	HA1604	ET4
13	HA18021	HA1604	ET4
14	HA18021	HA1604	ET4
15	HA18021	HA1604	ET4
16	HA18021	HA1604	ET4
17	HA18021	HA1604	ET4
18	HA18021	HA1604	ET4
19	HA18021	HA1604	ET4
20	HA18021	HA1604	ET4
21	HA18021	HA1604	ET4
22	HA18021	HA1604	ET4
23	HA18021	HA1604	ET4
24	HA18021	HA1604	ET4
25	HA18021	HA1604	ET4
26	HA18021	HA1604	ET4
27	HA18021	HA1604	ET4
28	HA18021	HA1604	ET4
29	HA18021	HA1604	ET4
30	HA18021	HA1604	ET4
31	HA18021	HA1604	ET4
32	HA18021	HA1604	ET4
33	HA18021	HA1604	ET4
34	HA18021	HA1604	ET4
35	HA18021	HA1604	ET4
36	HA18021	HA1604	ET4
37	HA18021	HA1604	ET4
38	HA18021	HA1604	ET4
39	HA18021	HA1604	ET4
40	HA18021	HA1604	ET4
41	HA18021	HA1604	ET4
42	HA18021	HA1604	ET4
43	HA18021	HA1604	ET4
44	HA18021	HA1604	ET4
45	HA18021	HA1604	ET4
46	HA18021	HA1604	ET4
47	HA18021	HA1604	ET4
48	HA18021	HA1604	ET4
49	HA18021	HA1604	ET4
50	HA18021	HA1604	ET4
51	HA18021	HA1604	ET4
52	HA18021	HA1604	ET4
53	HA18021	HA1604	ET4
54	HA18021	HA1604	ET4
55	HA18021	HA1604	ET4
56	HA18021	HA1604	ET4
57	HA18021	HA1604	ET4
58	HA18021	HA1604	ET4
59	HA18021	HA1604	ET4
60	HA18021	HA1604	ET4
61	HA18021	HA1604	ET4
62	HA18021	HA1604	ET4
63	HA18021	HA1604	ET4
64	HA18021	HA1604	ET4
65	HA18021	HA1604	ET4
66	HA18021	HA1604	ET4
67	HA18021	HA1604	ET4
68	HA18021	HA1604	ET4
69	HA18021	HA1604	ET4
70	HA18021	HA1604	ET4
71	HA18021	HA1604	ET4
72	HA18021	HA1604	ET4
73	HA18021	HA1604	ET4
74	HA18021	HA1604	ET4
75	HA18021	HA1604	ET4
76	HA18021	HA1604	ET4
77	HA18021	HA1604	ET4
78	HA18021	HA1604	ET4
79	HA18021	HA1604	ET4
80	HA18021	HA1604	ET4
81	HA18021	HA1604	ET4
82	HA18021	HA1604	ET4
83	HA18021	HA1604	ET4
84	HA18021	HA1604	ET4
85	HA18021	HA1604	ET4
86	HA18021	HA1604	ET4
87	HA18021	HA1604	ET4
88	HA18021	HA1604	ET4
89	HA18021	HA1604	ET4
90	HA18021	HA1604	ET4
91	HA18021	HA1604	ET4
92	HA18021	HA1604	ET4
93	HA18021	HA1604	ET4
94	HA18021	HA1604	ET4
95	HA18021	HA1604	ET4
96	HA18021	HA1604	ET4
97	HA18021	HA1604	ET4
98	HA18021	HA1604	ET4
99	HA18021	HA1604	ET4
100	HA18021	HA1604	ET4

FIGURE 3 (CONT.)

2454	AA32939	EST: RC_AA32939	
4556	V02741	H110041	EST
21444	AA32102	H147705	EST: Yeasty similar to F3949 3' C. elegans
8620	AT00015	H147705	EST: Yeasty similar to F3949 3' C. elegans
30037	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
3380	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
25640	AA32939	H147705	EST: Yeasty similar to F3949 3' C. elegans
46477	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
30882	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
18620	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
9607	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
13965	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
28143	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
33082	AA42254	H147705	EST: Yeasty similar to F3949 3' C. elegans
37020	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
786	AA32939	H147705	EST: Yeasty similar to F3949 3' C. elegans
16073	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
3457	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
24752	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
11751	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
24822	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
18752	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
42290	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
10087	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
30872	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
23096	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
4586	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
30816	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
28758	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
30786	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
7097	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
34452	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
34528	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
21431	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
11342	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
4487	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans
11454	H147705	H147705	EST: Yeasty similar to F3949 3' C. elegans

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FIGURE 3 (CONT.)

[illegible]

FIGURE 3 (CONT.)

[illegible]

FIGURE 3 (CONT.)

[illegible]

FIGURE 3 (CONT.)

8112	30	A432862	Hs 104558	EST1
8113	30	A432863	Hs 104559	EST1
32236	30	B44237	Hs 51435	Natural melanocyte-associated macropiggy protein 2
32719	30	U94053	Hs 54652	DITHIOCARPATE (DIPYD) TOXINASE PRECURSOR
32720	30	A432864	Hs 104560	EST1
37972	30	A432865	Hs 104561	EST1
41266	30	R31377	Hs 30566	EST1
41267	30	R31378	Hs 30567	EST1
23189	30	A432866	Hs 113252	EST1
29851	30	I227145	Hs A5984	EST1
32861	30	U522719	Hs 522719	EST1

FIGURE 4

[illegible]

FIGURE 4 (CONT.)

[illegible]

FIGURE 4 (CONT.)

35093	AA45486	Hs 05854	EST, Weakly similar to protein b1 complex (rat-specific protein [C antigen])
35094	AA450715	Hs 107478	ESTs
1806	L19520	Hs 30850	ME-ARIMA-ASSOCIATED ANTIGEN 2
35095	AA450716	Hs 30850	ME-ARIMA-ASSOCIATED ANTIGEN 2
35096	AA4512	Hs 22143	ESTs, Weakly similar to Hs 11413 CLASS 3 WARNING ENTRY (H sapiens)
35097	AA450717	Hs 55896	ESTs, Weakly similar to polyphospho H acetylglutamate synthetase (H sapiens)
35098	AA450718	Hs 55896	ESTs
35099	AA450719	Hs 55896	ESTs
35100	AA450720	Hs 55896	ESTs
35101	AA450721	Hs 55896	ESTs
35102	AA450722	Hs 55896	ESTs
35103	AA450723	Hs 55896	ESTs
35104	AA450724	Hs 55896	ESTs
35105	AA450725	Hs 55896	ESTs
35106	AA450726	Hs 55896	ESTs
35107	AA450727	Hs 55896	ESTs
35108	AA450728	Hs 55896	ESTs
35109	AA450729	Hs 55896	ESTs
35110	AA450730	Hs 55896	ESTs
35111	AA450731	Hs 55896	ESTs
35112	AA450732	Hs 55896	ESTs
35113	AA450733	Hs 55896	ESTs
35114	AA450734	Hs 55896	ESTs
35115	AA450735	Hs 55896	ESTs
35116	AA450736	Hs 55896	ESTs
35117	AA450737	Hs 55896	ESTs
35118	AA450738	Hs 55896	ESTs
35119	AA450739	Hs 55896	ESTs
35120	AA450740	Hs 55896	ESTs
35121	AA450741	Hs 55896	ESTs
35122	AA450742	Hs 55896	ESTs
35123	AA450743	Hs 55896	ESTs
35124	AA450744	Hs 55896	ESTs
35125	AA450745	Hs 55896	ESTs
35126	AA450746	Hs 55896	ESTs
35127	AA450747	Hs 55896	ESTs
35128	AA450748	Hs 55896	ESTs
35129	AA450749	Hs 55896	ESTs
35130	AA450750	Hs 55896	ESTs
35131	AA450751	Hs 55896	ESTs
35132	AA450752	Hs 55896	ESTs
35133	AA450753	Hs 55896	ESTs
35134	AA450754	Hs 55896	ESTs
35135	AA450755	Hs 55896	ESTs
35136	AA450756	Hs 55896	ESTs
35137	AA450757	Hs 55896	ESTs
35138	AA450758	Hs 55896	ESTs
35139	AA450759	Hs 55896	ESTs
35140	AA450760	Hs 55896	ESTs
35141	AA450761	Hs 55896	ESTs
35142	AA450762	Hs 55896	ESTs
35143	AA450763	Hs 55896	ESTs
35144	AA450764	Hs 55896	ESTs
35145	AA450765	Hs 55896	ESTs
35146	AA450766	Hs 55896	ESTs
35147	AA450767	Hs 55896	ESTs
35148	AA450768	Hs 55896	ESTs
35149	AA450769	Hs 55896	ESTs
35150	AA450770	Hs 55896	ESTs
35151	AA450771	Hs 55896	ESTs
35152	AA450772	Hs 55896	ESTs
35153	AA450773	Hs 55896	ESTs
35154	AA450774	Hs 55896	ESTs
35155	AA450775	Hs 55896	ESTs
35156	AA450776	Hs 55896	ESTs
35157	AA450777	Hs 55896	ESTs
35158	AA450778	Hs 55896	ESTs
35159	AA450779	Hs 55896	ESTs
35160	AA450780	Hs 55896	ESTs
35161	AA450781	Hs 55896	ESTs
35162	AA450782	Hs 55896	ESTs
35163	AA450783	Hs 55896	ESTs
35164	AA450784	Hs 55896	ESTs
35165	AA450785	Hs 55896	ESTs
35166	AA450786	Hs 55896	ESTs
35167	AA450787	Hs 55896	ESTs
35168	AA450788	Hs 55896	ESTs
35169	AA450789	Hs 55896	ESTs
35170	AA450790	Hs 55896	ESTs
35171	AA450791	Hs 55896	ESTs
35172	AA450792	Hs 55896	ESTs
35173	AA450793	Hs 55896	ESTs
35174	AA450794	Hs 55896	ESTs
35175	AA450795	Hs 55896	ESTs
35176	AA450796	Hs 55896	ESTs
35177	AA450797	Hs 55896	ESTs
35178	AA450798	Hs 55896	ESTs
35179	AA450799	Hs 55896	ESTs
35180	AA450800	Hs 55896	ESTs
35181	AA450801	Hs 55896	ESTs
35182	AA450802	Hs 55896	ESTs
35183	AA450803	Hs 55896	ESTs
35184	AA450804	Hs 55896	ESTs
35185	AA450805	Hs 55896	ESTs
35186	AA450806	Hs 55896	ESTs
35187	AA450807	Hs 55896	ESTs
35188	AA450808	Hs 55896	ESTs
35189	AA450809	Hs 55896	ESTs
35190	AA450810	Hs 55896	ESTs
35191	AA450811	Hs 55896	ESTs
35192	AA450812	Hs 55896	ESTs
35193	AA450813	Hs 55896	ESTs
35194	AA450814	Hs 55896	ESTs
35195	AA450815	Hs 55896	ESTs
35196	AA450816	Hs 55896	ESTs
35197	AA450817	Hs 55896	ESTs
35198	AA450818	Hs 55896	ESTs
35199	AA450819	Hs 55896	ESTs
35200	AA450820	Hs 55896	ESTs
35201	AA450821	Hs 55896	ESTs
35202	AA450822	Hs 55896	ESTs
35203	AA450823	Hs 55896	ESTs
35204	AA450824	Hs 55896	ESTs
35205	AA450825	Hs 55896	ESTs
35206	AA450826	Hs 55896	ESTs
35207	AA450827	Hs 55896	ESTs
35208	AA450828	Hs 55896	ESTs
35209	AA450829	Hs 55896	ESTs
35210	AA450830	Hs 55896	ESTs
35211	AA450831	Hs 55896	ESTs
35212	AA450832	Hs 55896	ESTs
35213	AA450833	Hs 55896	ESTs
35214	AA450834	Hs 55896	ESTs
35215	AA450835	Hs 55896	ESTs
35216	AA450836	Hs 55896	ESTs
35217	AA450837	Hs 55896	ESTs
35218	AA450838	Hs 55896	ESTs
35219	AA450839	Hs 55896	ESTs
35220	AA450840	Hs 55896	ESTs
35221	AA450841	Hs 55896	ESTs
35222	AA450842	Hs 55896	ESTs

FIGURE 4 (CONT.)

39265	1	U1254	Hs.3255	EST1	Hs.3255	EST1
4102	2	U1280	Hs.13474	Human, D2 pro-oncogene receptor (PTC2R) mRNA, partial cds	Hs.13474	Human, D2 pro-oncogene receptor (PTC2R) mRNA, partial cds
4507	3	U41955	Hs.24502	Human, putative calcium influx channel (hca2) mRNA, complete cds	Hs.24502	Human, putative calcium influx channel (hca2) mRNA, complete cds
35006	4	AA023227	Hs.97345	EST's moderately similar to Hs.109004b (R. norvegicus)	Hs.97345	EST's moderately similar to Hs.109004b (R. norvegicus)
17272	5	U41956	Hs.21801	EST1	Hs.21801	EST1
14837	6	U41957	Hs.21801	EST1	Hs.21801	EST1
17326	9	AA059585	Hs.41175	EST1	Hs.41175	EST1
256495	10	U41958	Hs.40975	EST1	Hs.40975	EST1
256496	11	U41959	Hs.40975	EST1	Hs.40975	EST1
17997	12	AA16953	Hs.74855	EST1	Hs.74855	EST1
13983	13	AA170017	Hs.34527	EST's moderately similar to Hs.41156 (H. sapiens)	Hs.34527	EST's moderately similar to Hs.41156 (H. sapiens)
20335	14	AA25102	Hs.48954	EST1	Hs.48954	EST1
42612	15	AB419	Hs.53369	EST1	Hs.53369	EST1
503	16	D96070	Hs.96	ATL-derived PAK-responsive (APR) peptide	Hs.96	ATL-derived PAK-responsive (APR) peptide
10124	17	U41960	Hs.3255	EST1	Hs.3255	EST1
10266	18	AA020457	Hs.32497	EST1	Hs.32497	EST1
25652	19	U41961	Hs.32497	EST1	Hs.32497	EST1
7736	20	AA023721	Hs.19651	Human, tyrosyl-DNA synthase mRNA, complete cds	Hs.19651	Human, tyrosyl-DNA synthase mRNA, complete cds
39939	21	Hs.3454	Hs.11929	EST - RC_193454	Hs.11929	EST - RC_193454
27014	22	AA054475	Hs.32733	EST's weakly similar to CBEL3.3 (C. elegans)	Hs.32733	EST's weakly similar to CBEL3.3 (C. elegans)
21655	23	U41962	Hs.82925	Human, transposon (TR) mRNA, complete cds	Hs.82925	Human, transposon (TR) mRNA, complete cds
37253	24	AA48357	Hs.10324	EST1	Hs.10324	EST1
38624	25	F10936	Hs.17731	EST1	Hs.17731	EST1
32479	26	U41963	Hs.17731	EST1	Hs.17731	EST1
32479	27	U41964	Hs.17731	EST1	Hs.17731	EST1
32479	28	U41965	Hs.17731	EST1	Hs.17731	EST1
32479	29	U41966	Hs.17731	EST1	Hs.17731	EST1
32479	30	U41967	Hs.17731	EST1	Hs.17731	EST1
32479	31	U41968	Hs.17731	EST1	Hs.17731	EST1
32479	32	U41969	Hs.17731	EST1	Hs.17731	EST1
32479	33	U41970	Hs.17731	EST1	Hs.17731	EST1
32479	34	U41971	Hs.17731	EST1	Hs.17731	EST1
32479	35	U41972	Hs.17731	EST1	Hs.17731	EST1
32479	36	U41973	Hs.17731	EST1	Hs.17731	EST1
32479	37	U41974	Hs.17731	EST1	Hs.17731	EST1
32479	38	U41975	Hs.17731	EST1	Hs.17731	EST1
32479	39	U41976	Hs.17731	EST1	Hs.17731	EST1
32479	40	U41977	Hs.17731	EST1	Hs.17731	EST1
32479	41	U41978	Hs.17731	EST1	Hs.17731	EST1
32479	42	U41979	Hs.17731	EST1	Hs.17731	EST1
32479	43	U41980	Hs.17731	EST1	Hs.17731	EST1
32479	44	U41981	Hs.17731	EST1	Hs.17731	EST1
32479	45	U41982	Hs.17731	EST1	Hs.17731	EST1
32479	46	U41983	Hs.17731	EST1	Hs.17731	EST1
32479	47	U41984	Hs.17731	EST1	Hs.17731	EST1
32479	48	U41985	Hs.17731	EST1	Hs.17731	EST1
32479	49	U41986	Hs.17731	EST1	Hs.17731	EST1
32479	50	U41987	Hs.17731	EST1	Hs.17731	EST1
32479	51	U41988	Hs.17731	EST1	Hs.17731	EST1
32479	52	U41989	Hs.17731	EST1	Hs.17731	EST1
32479	53	U41990	Hs.17731	EST1	Hs.17731	EST1
32479	54	U41991	Hs.17731	EST1	Hs.17731	EST1
32479	55	U41992	Hs.17731	EST1	Hs.17731	EST1
32479	56	U41993	Hs.17731	EST1	Hs.17731	EST1
32479	57	U41994	Hs.17731	EST1	Hs.17731	EST1
32479	58	U41995	Hs.17731	EST1	Hs.17731	EST1
32479	59	U41996	Hs.17731	EST1	Hs.17731	EST1
32479	60	U41997	Hs.17731	EST1	Hs.17731	EST1
32479	61	U41998	Hs.17731	EST1	Hs.17731	EST1
32479	62	U41999	Hs.17731	EST1	Hs.17731	EST1
32479	63	U42000	Hs.17731	EST1	Hs.17731	EST1
32479	64	U42001	Hs.17731	EST1	Hs.17731	EST1
32479	65	U42002	Hs.17731	EST1	Hs.17731	EST1
32479	66	U42003	Hs.17731	EST1	Hs.17731	EST1
32479	67	U42004	Hs.17731	EST1	Hs.17731	EST1
32479	68	U42005	Hs.17731	EST1	Hs.17731	EST1
32479	69	U42006	Hs.17731	EST1	Hs.17731	EST1
32479	70	U42007	Hs.17731	EST1	Hs.17731	EST1
32479	71	U42008	Hs.17731	EST1	Hs.17731	EST1
32479	72	U42009	Hs.17731	EST1	Hs.17731	EST1
32479	73	U42010	Hs.17731	EST1	Hs.17731	EST1
32479	74	U42011	Hs.17731	EST1	Hs.17731	EST1
32479	75	U42012	Hs.17731	EST1	Hs.17731	EST1
32479	76	U42013	Hs.17731	EST1	Hs.17731	EST1
32479	77	U42014	Hs.17731	EST1	Hs.17731	EST1
32479	78	U42015	Hs.17731	EST1	Hs.17731	EST1
32479	79	U42016	Hs.17731	EST1	Hs.17731	EST1
32479	80	U42017	Hs.17731	EST1	Hs.17731	EST1
32479	81	U42018	Hs.17731	EST1	Hs.17731	EST1
32479	82	U42019	Hs.17731	EST1	Hs.17731	EST1
32479	83	U42020	Hs.17731	EST1	Hs.17731	EST1
32479	84	U42021	Hs.17731	EST1	Hs.17731	EST1
32479	85	U42022	Hs.17731	EST1	Hs.17731	EST1
32479	86	U42023	Hs.17731	EST1	Hs.17731	EST1
32479	87	U42024	Hs.17731	EST1	Hs.17731	EST1
32479	88	U42025	Hs.17731	EST1	Hs.17731	EST1
32479	89	U42026	Hs.17731	EST1	Hs.17731	EST1
32479	90	U42027	Hs.17731	EST1	Hs.17731	EST1
32479	91	U42028	Hs.17731	EST1	Hs.17731	EST1
32479	92	U42029	Hs.17731	EST1	Hs.17731	EST1
32479	93	U42030	Hs.17731	EST1	Hs.17731	EST1
32479	94	U42031	Hs.17731	EST1	Hs.17731	EST1
32479	95	U42032	Hs.17731	EST1	Hs.17731	EST1
32479	96	U42033	Hs.17731	EST1	Hs.17731	EST1
32479	97	U42034	Hs.17731	EST1	Hs.17731	EST1
32479	98	U42035	Hs.17731	EST1	Hs.17731	EST1
32479	99	U42036	Hs.17731	EST1	Hs.17731	EST1
32479	100	U42037	Hs.17731	EST1	Hs.17731	EST1
32479	101	U42038	Hs.17731	EST1	Hs.17731	EST1
32479	102	U42039	Hs.17731	EST1	Hs.17731	EST1
32479	103	U42040	Hs.17731	EST1	Hs.17731	EST1
32479	104	U42041	Hs.17731	EST1	Hs.17731	EST1
32479	105	U42042	Hs.17731	EST1	Hs.17731	EST1
32479	106	U42043	Hs.17731	EST1	Hs.17731	EST1
32479	107	U42044	Hs.17731	EST1	Hs.17731	EST1
32479	108	U42045	Hs.17731	EST1	Hs.17731	EST1
32479	109	U42046	Hs.17731	EST1	Hs.17731	EST1
32479	110	U42047	Hs.17731	EST1	Hs.17731	EST1
32479	111	U42048	Hs.17731	EST1	Hs.17731	EST1
32479	112	U42049	Hs.17731	EST1	Hs.17731	EST1
32479	113	U42050	Hs.17731	EST1	Hs.17731	EST1
32479	114	U42051	Hs.17731	EST1	Hs.17731	EST1
32479	115	U42052	Hs.17731	EST1	Hs.17731	EST1
32479	116	U42053	Hs.17731	EST1	Hs.17731	EST1
32479	117	U42054	Hs.17731	EST1	Hs.17731	EST1
32479	118	U42055	Hs.17731	EST1	Hs.17731	EST1
32479	119	U42056	Hs.17731	EST1	Hs.17731	EST1
32479	120	U42057	Hs.17731	EST1	Hs.17731	EST1
32479	121	U42058	Hs.17731	EST1	Hs.17731	EST1
32479	122	U42059	Hs.17731	EST1	Hs.17731	EST1
32479	123	U42060	Hs.17731	EST1	Hs.17731	EST1
32479	124	U42061	Hs.17731	EST1	Hs.17731	EST1
32479	125	U42062	Hs.17731	EST1	Hs.17731	EST1
32479	126	U42063	Hs.17731	EST1	Hs.17731	EST1
32479	127	U42064	Hs.17731	EST1	Hs.17731	EST1
32479	128	U42065	Hs.17731	EST1	Hs.17731	EST1
32479	129	U42066	Hs.17731	EST1	Hs.17731	EST1
32479	130	U42067	Hs.17731	EST1	Hs.17731	EST1
32479	131	U42068	Hs.17731	EST1	Hs.17731	EST1
32479	132	U42069	Hs.17731	EST1	Hs.17731	EST1
32479	133	U42070	Hs.17731	EST1	Hs.17731	EST1
32479	134	U42071	Hs.17731	EST1	Hs.17731	EST1
32479	135	U42072	Hs.17731	EST1	Hs.17731	EST1
32479	136	U42073	Hs.17731	EST1	Hs.17731	EST1
32479	137	U42074	Hs.17731	EST1	Hs.17731	EST1
32479	138	U42075	Hs.17731	EST1	Hs.17731	EST1
32479	139	U42076	Hs.17731	EST1	Hs.17731	EST1
32479	140	U42077	Hs.17731	EST1	Hs.17731	EST1
32479	141	U42078	Hs.17731	EST1	Hs.17731	EST1
32479	142	U42079	Hs.17731	EST1	Hs.17731	EST1
32479	143	U42080	Hs.17731	EST1	Hs.17731	EST1
32479	144	U42081	Hs.17731	EST1	Hs.17731	EST1
32479	145	U42082	Hs.17731	EST1	Hs.17731	EST1
32479	146	U42083	Hs.17731	EST1	Hs.17731	EST1
32479	147	U42084	Hs.17731	EST1	Hs.17731	EST1
32479	148	U42085	Hs.17731	EST1	Hs.17731	EST1
32479	149	U42086	Hs.17731	EST1	Hs.17731	EST1
32479	150	U42087	Hs.17731	EST1	Hs.17731	EST1
32479	151	U42088	Hs.17731	EST1	Hs.17731	EST1
32479	152	U42089	Hs.17731	EST1	Hs.17731	EST1
32479	153	U42090	Hs.17731	EST1	Hs.17731	EST1
32479	154	U42091	Hs.17731	EST1	Hs.17731	EST1
32479	155	U42092	Hs.17731	EST1	Hs.17731	EST1
32479	156	U42093	Hs.17731	EST1	Hs.17731	EST1
32479	157	U42094	Hs.17731	EST1	Hs.17731	EST1
32479	158	U42095	Hs.17731	EST1	Hs.17731	EST1
32479	159	U42096	Hs.17731	EST1	Hs.17731	EST1
32479	160	U42097	Hs.17731	EST1	Hs.17731	EST1
32479	161	U42098	Hs.17731	EST1	Hs.17731	EST1
32479	162	U42099	Hs.17731	EST1	Hs.17731	EST1
32479	163	U42100	Hs.17731	EST1	Hs.17731	EST1
32479	164	U42101	Hs.17731	EST1	Hs.17731	EST1
32479	165	U42102	Hs.17731	EST1	Hs.17731	EST1
32479	166	U42103	Hs.17731	EST1	Hs.17731	EST1
32479	167	U42104	Hs.17731	EST1	Hs.17731	EST1
32479	168	U42105	Hs.17731	EST1	Hs.17731	EST1

FIGURE 4 (CONT.)

3	8	AA621323	Hs.110432	EST1	
3	8	AA621321	Hs.81668	EST1	
3	8	AA621320	Hs.70305	Human plasmin (CD33) cDNA complete cds	
3	8	AA621319	Hs.70305	Human plasmin (CD33) cDNA complete cds	
3	8	AA621318	Hs.103331	EST - RC_A050907	
3	8	AA621317	Hs.103331	EST1	
3	8	AA621316	Hs.50515	Human rRNA for 16S/16S gene partial cds	
3	8	AA621315	Hs.13068	EST1	
3	8	AA621314	Hs.13068	EST1	
3	8	AA621313	Hs.13068	EST1	
3	8	AA621312	Hs.13068	EST1	
3	8	AA621311	Hs.13068	EST1	
3	8	AA621310	Hs.13068	EST1	
3	8	AA621309	Hs.13068	EST1	
3	8	AA621308	Hs.13068	EST1	
3	8	AA621307	Hs.13068	EST1	
3	8	AA621306	Hs.13068	EST1	
3	8	AA621305	Hs.13068	EST1	
3	8	AA621304	Hs.13068	EST1	
3	8	AA621303	Hs.13068	EST1	
3	8	AA621302	Hs.13068	EST1	
3	8	AA621301	Hs.13068	EST1	
3	8	AA621300	Hs.13068	EST1	
3	8	AA621299	Hs.13068	EST1	
3	8	AA621298	Hs.13068	EST1	
3	8	AA621297	Hs.13068	EST1	
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3	8	AA621289	Hs.13068	EST1	
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3	8	AA621286	Hs.13068	EST1	
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3	8	AA621280	Hs.13068	EST1	
3	8	AA621279	Hs.13068	EST1	
3	8	AA621278	Hs.13068	EST1	
3	8	AA621277	Hs.13068	EST1	
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3	8	AA621273	Hs.13068	EST1	
3	8	AA621272	Hs.13068	EST1	
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3	8	AA621270	Hs.13068	EST1	
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3	8	AA621263	Hs.13068	EST1	
3	8	AA621262	Hs.13068	EST1	
3	8	AA621261	Hs.13068	EST1	
3	8	AA621260	Hs.13068	EST1	
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3	8	AA621256	Hs.13068	EST1	
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3	8	AA621251	Hs.13068	EST1	
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3	8	AA621249	Hs.13068	EST1	
3	8	AA621248	Hs.13068	EST1	
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3	8	AA621246	Hs.13068	EST1	
3	8	AA621245	Hs.13068	EST1	
3	8	AA621244	Hs.13068	EST1	
3	8	AA621243	Hs.13068	EST1	
3	8	AA621242	Hs.13068	EST1	
3	8	AA621241	Hs.13068	EST1	
3	8	AA621240	Hs.13068	EST1	
3	8	AA621239	Hs.13068	EST1	
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3	8	AA621237	Hs.13068	EST1	
3	8	AA621236	Hs.13068	EST1	
3	8	AA621235	Hs.13068	EST1	
3	8	AA621234	Hs.13068	EST1	
3	8	AA621233	Hs.13068	EST1	
3	8	AA621232	Hs.13068	EST1	
3	8	AA621231	Hs.13068	EST1	
3	8	AA621230	Hs.13068	EST1	
3	8	AA621229	Hs.13068	EST1	
3	8	AA621228	Hs.13068	EST1	
3	8	AA621227	Hs.13068	EST1	
3	8	AA621226	Hs.13068	EST1	
3	8	AA621225	Hs.13068	EST1	
3	8	AA621224	Hs.13068	EST1	
3	8	AA621223	Hs.13068	EST1	
3	8	AA621222	Hs.13068	EST1	
3	8	AA621221	Hs.13068	EST1	
3	8	AA621220	Hs.13068	EST1	
3	8	AA621219	Hs.13068	EST1	
3	8	AA621218	Hs.13068	EST1	
3	8	AA621217	Hs.13068	EST1	
3	8	AA621216	Hs.13068	EST1	
3	8	AA621215	Hs.13068	EST1	
3	8	AA621214	Hs.13068	EST1	
3	8	AA621213	Hs.13068	EST1	
3	8	AA621212	Hs.13068	EST1	
3	8	AA621211	Hs.13068	EST1	
3	8	AA621210	Hs.13068	EST1	
3	8	AA621209	Hs.13068	EST1	
3	8	AA621208	Hs.13068	EST1	
3	8	AA621207	Hs.13068	EST1	
3	8	AA621206	Hs.13068	EST1	
3	8	AA621205	Hs.13068	EST1	
3	8	AA621204	Hs.13068	EST1	
3	8	AA621203	Hs.13068	EST1	
3	8	AA621202	Hs.13068	EST1	
3	8	AA621201	Hs.13068	EST1	
3	8	AA621200	Hs.13068	EST1	
3	8	AA621199	Hs.13068	EST1	
3	8	AA621198	Hs.13068	EST1	
3	8	AA621197	Hs.13068	EST1	
3	8	AA621196	Hs.13068	EST1	
3	8	AA621195	Hs.13068	EST1	
3	8	AA621194	Hs.13068	EST1	
3	8	AA621193	Hs.13068	EST1	
3	8	AA621192	Hs.13068	EST1	
3	8	AA621191	Hs.13068	EST1	
3	8	AA621190	Hs.13068	EST1	
3	8	AA621189	Hs.13068	EST1	
3	8	AA621188	Hs.13068	EST1	
3	8	AA621187	Hs.13068	EST1	
3	8	AA621186	Hs.13068	EST1	
3	8	AA621185	Hs.13068	EST1	
3	8	AA621184	Hs.13068	EST1	
3	8	AA621183	Hs.13068	EST1	
3	8	AA621182	Hs.13068	EST1	
3	8	AA621181	Hs.13068	EST1	
3	8	AA621180	Hs.13068	EST1	
3	8	AA621179	Hs.13068	EST1	
3	8	AA621178	Hs.13068	EST1	
3	8	AA621177	Hs.13068	EST1	
3	8	AA621176	Hs.13068	EST1	
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3	8	AA621174	Hs.13068	EST1	
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3	8	AA621170	Hs.13068	EST1	
3	8	AA621169	Hs.13068	EST1	
3	8	AA621168	Hs.13068	EST1	
3	8	AA621167	Hs.13068	EST1	
3	8	AA621166	Hs.13068	EST1	
3	8	AA621165	Hs.13068	EST1	
3	8	AA621164	Hs.13068	EST1	
3	8	AA621163	Hs.13068	EST1	
3	8	AA621162	Hs.13068	EST1	
3	8	AA621161	Hs.13068	EST1	
3	8	AA621160	Hs.13068	EST1	
3	8	AA621159	Hs.13068	EST1	
3	8	AA621158	Hs.13068	EST1	
3	8	AA621157	Hs.13068	EST1	
3	8	AA621156	Hs.13068	EST1	
3	8	AA621155	Hs.13068	EST1	
3	8	AA621154	Hs.13068	EST1	
3	8	AA621153	Hs.13068	EST1	
3	8	AA621152	Hs.13068	EST1	
3	8	AA621151	Hs.13068	EST1	
3	8	AA621150	Hs.13068	EST1	
3	8	AA621149	Hs.13068	EST1	
3	8	AA621148	Hs.13068	EST1	
3	8	AA621147	Hs.13068	EST1	
3	8	AA621146	Hs.13068	EST1	
3	8	AA621145	Hs.13068	EST1	
3	8	AA621144	Hs.13068	EST1	
3	8	AA621143	Hs.13068	EST1	
3	8	AA621142	Hs.13068	EST1	
3	8	AA621141	Hs.13068	EST1	
3	8	AA621140	Hs.13068	EST1	
3	8	AA621139	Hs.13068	EST1	
3	8	AA621138	Hs.13068	EST1	
3	8	AA621137	Hs.13068	EST1	
3	8	AA621136	Hs.13068	EST1	
3	8	AA621135	Hs.13068	EST1	
3	8	AA621134	Hs.13068	EST1	
3	8	AA621133	Hs.13068	EST1	
3	8	AA621132	Hs.13068	EST1	
3	8	AA621131	Hs.13068	EST1	
3	8	AA621130	Hs.13068	EST1	
3	8	AA621129	Hs.13068	EST1	
3	8	AA621128	Hs.13068	EST1	
3	8	AA621127	Hs.13068	EST1	
3	8	AA621126	Hs.13068	EST1	
3	8	AA621125	Hs.13068	EST1	
3	8	AA621124	Hs.13068	EST1	
3	8	AA621123	Hs.13068	EST1	
3	8	AA621122	Hs.13068	EST1	
3	8	AA621121	Hs.13068	EST1	
3	8	AA621120	Hs.13068	EST1	
3	8	AA621119	Hs.13068	EST1	
3	8	AA621118	Hs.13068	EST1	
3	8	AA621117	Hs.13068	EST1	
3	8	AA621116	Hs.13068	EST1	
3	8	AA621115	Hs.13068	EST1	
3	8	AA621114	Hs.13068	EST1	
3	8	AA621113	Hs.13068	EST1	
3	8	AA621112	Hs.13068	EST1	
3	8	AA621111	Hs.13068	EST1	
3	8	AA621110	Hs.13068	EST1	
3	8	AA621109	Hs.13068	EST1	
3	8	AA621108	Hs.13068	EST1	
3	8	AA621107	Hs.13068	EST1	
3	8	AA621106	Hs.13068	EST1	
3	8	AA621105	Hs.13068	EST1	
3	8	AA621104	Hs.13068	EST1	
3	8	AA621103	Hs.13068	EST1	
3	8	AA621102	Hs.13068	EST1	
3	8	AA621101	Hs.13068	EST1	
3	8	AA621100	Hs.13068	EST1	
3	8	AA621099	Hs.13068	EST1	
3	8	AA621098	Hs.13068	EST1	
3	8	AA621097	Hs.13068	EST1	
3	8	AA621096	Hs.13068	EST1	
3	8	AA621095	Hs.13068	EST1	
3	8	AA621094	Hs.13068	EST1	
3	8	AA621093	Hs.13068	EST1	
3	8	AA621092	Hs.13068	EST1	
3	8	AA621091	Hs.13068	EST1	
3	8	AA621090	Hs.13068	EST1	
3	8	AA621089	Hs.13068	EST1	
3	8	AA621088	Hs.13068	EST1	
3	8	AA621087	Hs.13068	EST1	
3	8	AA621086	Hs.13068	EST1	
3	8	AA621085	Hs.13068	EST1	
3	8	AA621084	Hs.13068	EST1	
3	8	AA621083	Hs.13068	EST1	
3	8	AA621082	Hs.13068	EST1	
3	8	AA621081	Hs.13068	EST1	</

FIGURE 4 (CONT.)

11640	AA158132	Hs 11617	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
11641	AA158133	Hs 11618	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
15962	AA158134	Hs 11619	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
13229	AA158135	Hs 11620	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
27115	AA158136	Hs 11621	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
17715	AA158137	Hs 11622	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
17925	AA158138	Hs 11623	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
5253	AA158139	Hs 11624	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
17167	AA158140	Hs 11625	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
26330	AA158141	Hs 11626	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
22950	AA158142	Hs 11627	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
7445	AA158143	Hs 11628	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
19255	AA158144	Hs 11629	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
7392	AA158145	Hs 11630	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
30647	AA158146	Hs 11631	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
41664	AA158147	Hs 11632	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
19174	AA158148	Hs 11633	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
32620	AA158149	Hs 11634	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
41077	AA158150	Hs 11635	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
38156	AA158151	Hs 11636	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
32156	AA158152	Hs 11637	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
19177	AA158153	Hs 11638	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
6036	AA158154	Hs 11639	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
1825	AA158155	Hs 11640	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
10773	AA158156	Hs 11641	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
21009	AA158157	Hs 11642	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
36200	AA158158	Hs 11643	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
8004	AA158159	Hs 11644	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
12131	AA158160	Hs 11645	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
5928	AA158161	Hs 11646	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
19177	AA158162	Hs 11647	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
19987	AA158163	Hs 11648	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
6261	AA158164	Hs 11649	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
13251	AA158165	Hs 11650	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
33615	AA158166	Hs 11651	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
2028	AA158167	Hs 11652	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
21109	AA158168	Hs 11653	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
4189	AA158169	Hs 11654	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
17018	AA158170	Hs 11655	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
25345	AA158171	Hs 11656	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
8159	AA158172	Hs 11657	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
33035	AA158173	Hs 11658	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
3127	AA158174	Hs 11659	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
11977	AA158175	Hs 11660	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]
32930	AA158176	Hs 11661	EST1 highly similar to Y6A1 PROTEIN [Saccharomyces cerevisiae]

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FIGURE 4 (CONT.)

26	162512	Hs 6531	Human alpha2 (class 1460) unknown protein mRNA, partial cds.
27	162513	Hs 18262	ESTs
28	A2726820	Hs 35456	EST
29	V01506	Hs 35456	EST
30	Hs 35456	Hs 35456	EST
31	A412432	Hs 35456	EST
32	N52971	Hs 42118	ESTs
33	A448097	Hs 28555	ESTs
34	Hs 28555	Hs 28555	ESTs
35	D21182	Hs 75237	Human mRNA for KIAA0035 gene, partial cds.
36	X07788	Hs 84674	Haploids mRNA for fish protein
37	A448097	Hs 28555	ESTs
38	A448097	Hs 28555	ESTs
39	L21425	Hs 51181	ESTs
40	A442122	Hs 21706	ESTs
41	A449085	Hs 21706	ESTs
42	T03065	Hs 27047	ESTs
43	A4401274	Hs 31720	Human alpha2 mRNA binding protein Gp-42 (GPI-42P) mRNA, complete cds.
44	A4412238	Hs 20782	ESTs. Viabley similar to ORF2 consensus sequence encoding intronless and reverse transcriptase minus (Rtaesi) (R. congoensis)
45	A4412238	Hs 20782	ESTs. Viabley similar to ORF2 consensus sequence encoding intronless and reverse transcriptase minus (Rtaesi) (R. congoensis)
46	X72841	Hs 2715	Human mitochondrial cytochrome b (CYTB) mRNA, complete cds.
47	R44684	Hs 103182	ESTs
48	T10065	Hs 42714	Human alpha2 T15-antigen protein T15R2 mRNA, complete cds.
49	X09750	Hs 80077	Haploids mRNA for TGF protein
50	X78627	Hs 75206	Haploids mRNA for TGF protein
51	X78627	Hs 75206	Haploids mRNA for TGF protein
52	A4415533	Hs 67101	ESTs
53	A442595	Hs 67101	ESTs
54	W73139	Hs 85403	Human alpha2 protein-lysine kinase (EPH2) (EPH2) mRNA, complete cds.
55	A442595	Hs 67101	ESTs
56	A442595	Hs 67101	ESTs
57	T27857	Hs 21603	Human mRNA for KIAA0035 gene, complete cds.
58	A4443720	Hs 75651	ESTs
59	A4443720	Hs 75651	ESTs
60	H03132-NT3238	Hs 3426	EST - H03132-NT3238
61	H18927	Hs 815	Human tumor test c protein mRNA, complete cds.
62	A4431258	Hs 815	ESTs
63	A4431258	Hs 815	ESTs
64	Z35511	Hs 6738	ESTs. Viabley similar to PROBLEME ES PROTEIN (human peptidomimetic type 5)
65	N32078	Hs 13204	Human alpha2 mRNA for KIAA0037 protein, complete cds.
66	N32078	Hs 13204	Human alpha2 mRNA for KIAA0037 protein, complete cds.
67	D27716	Hs 10724	EST. Viabley similar to unknown (S. cerevisiae)
68	M83712	Hs 1814	Chlamydia-like protein (chlamydia-like protein) (S. cerevisiae)
69	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
70	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
71	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
72	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
73	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
74	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
75	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
76	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
77	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
78	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
79	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
80	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
81	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
82	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
83	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
84	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
85	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
86	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
87	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
88	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
89	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
90	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
91	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
92	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
93	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
94	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
95	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
96	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
97	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
98	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
99	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)
100	A4439344	Hs 10922	ESTs. Viabley similar to HYPOPHYSICAL 16.8 KDa PROTEIN IN SMY2/RS1 (S. cerevisiae)

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FIGURE 4 (CONT.)

30037	21	NP025	Hs 15028 EST1	Hs 15028 EST1	Weakly similar to MCB217 [C elegant]
27692	21	AA44202	Hs 15805 EST1	Hs 15805 EST1	Weakly similar to MCB217 [C elegant]
3350	23	55164	Hs 78320 EST1	Hs 78320 EST1	Weakly similar to MCB217 [C elegant]
42500	23	AA01186	Hs 10305 EST1	Hs 10305 EST1	Weakly similar to MCB217 [C elegant]
18620	34	70206	Hs 8411 EST1	Hs 8411 EST1	Weakly similar to MCB217 [C elegant]
15120	24	17324	Hs 8495 EST1	Hs 8495 EST1	Weakly similar to MCB217 [C elegant]
34723	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
17662	24	AA30177	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
11587	24	11587	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
32482	24	AA01186	Hs 8411 EST1	Hs 8411 EST1	Weakly similar to MCB217 [C elegant]
45	24	AA01186	Hs 8411 EST1	Hs 8411 EST1	Weakly similar to MCB217 [C elegant]
11701	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
10792	24	AA17367	Hs 10305 EST1	Hs 10305 EST1	Weakly similar to MCB217 [C elegant]
42200	24	70206	Hs 8411 EST1	Hs 8411 EST1	Weakly similar to MCB217 [C elegant]
28398	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
12990	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
36786	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
39462	24	AA00063	Hs 8072 EST1	Hs 8072 EST1	Weakly similar to MCB217 [C elegant]
22591	24	AA40008	Hs 10541 EST1	Hs 10541 EST1	Weakly similar to MCB217 [C elegant]
6387	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
11592	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
11464	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
33978	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
11853	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
22142	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
13532	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
32690	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
8103	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
14571	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
28169	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
20584	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
20557	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
21198	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
17362	24	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
11974	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
20796	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
46547	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
42022	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
365	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
26578	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
31898	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]
24028	23	AA30171	Hs 8507 EST1	Hs 8507 EST1	Weakly similar to MCB217 [C elegant]

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FIGURE 5

Primary Key	fold downregulated of Tumors	Accession	Ungene CLUSTER	Ungene Descriptor
2348	>10	M15556	Hs.75592	Adipose B fructose-bisphosphate
6463	>10	X97908	Hs.74126	H.sapiens mRNA for L-1p (L-BAP) protein
42139	>10	T73335	Hs.93194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48959	Hs.75950	H.sapiens mRNA for myosin light chain kinase
1353	>10	K02755	Hs.58512	COMPLEMENT C3 PRECURSOR
2426	>10	M19228	Hs.595	Apolipoprotein B (lipoaffecting Ag) antigen
8659	>10	A8022351	Hs.12557	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z38888	Hs.24192	ESTs
17810	>10	A4151402	Hs.48531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-III/unguanylin precursor
1304	>10	M15556	EST - HG4310-IT4590	
5960	>10	X67458	Hs.65424	Tetradactyl (glutathione-binding protein)
41967	>10	T41059	Hs.121713	Cyclochrome P450 subfamily XII (steroid 21-hydroxylase congenital adrenal hypoplasia)
24461	>10	M15557	Hs.307	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus
2372	>10	M15557	Hs.8952	Glutathione S-transferase A2
6001	>10	X6572	Hs.8552	Glutathione S-transferase A2
1750	>10	L10955	Hs.64485	Carbonic anhydrase IV
15130	>10	U77643	Hs.65455	Human sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402556	Hs.23264	EST - RC_R00594_5
41148	>10	R05984	EST - RC_R00594_5	Human chromosome (TECK) mRNA complete cds
31652	>10	N73558	Hs.50404	EST - U51010
4605	>10	U51010	ESTs	
28359	>10	AG089133	Hs.59115	ESTs
24096	>10	N32356	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.9352	ESTs
12084	>10	A0284767	Hs.21910	ESTs
41473	>10	R40732	Hs.11108	ESTs
27108	>10	AA043397	Hs.56114	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
2648	>10	M58266	Hs.32593	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR
19537	>10	F53270	Hs.32593	ESTs
18784	>10	F09746	Hs.71974	ESTs
5773	>10	X58162	Hs.73996	64 KD AUTOANTIGEN D1

FIGURE 5 (CONT.)

27387	AA125330	Hs.78254	ESTs
2866	M59815	Hs.76662	Complement component 4A
42530	W72859	Hs.74669	ESTs Weakly similar to SYNAPTOBREVIN 2 [H.sapiens]
827	D87433	Hs.84763	Human mRNA for KIAA0246 gene partial cds
650	D78014	Hs.74565	Human mRNA for dihydropyrimidinase related protein-3 complete cds
7026	Z80345	Hs.127610	Asyl-Coenzyme A dehydrogenase C2 to C-3 short chain
16735	AA045306	Hs.42956	ESTs
4630	U52101	Hs.9999	Human YMP mRNA complete cds
4655	U52959	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
42758	Z41411	Hs.107040	ESTs
35637	AA402533	Hs.22023	ESTs
40392	H96597	Hs.108680	ESTs
7354	AA023348	Hs.7858	ESTs
9034	CO1833	Hs.29759	ESTs Weakly similar to III ALU SUBFAMILY SX WARNING ENTRY III [H.sapiens]
10935	AA121334	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
5520	X06256	Hs.119219	Integrin alpha 5 (Btironectin receptor alpha polypeptide)
2547	M25609	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 5055kD isoform 1
5003	CO0608	Hs.107882	ESTs
41628	R70212	Hs.79530	Immunoglobulin-associated alpha
21934	R44449	Hs.48778	ESTs
11129	AA156673	Hs.15970	ESTs
40387	H99460	Hs.108673	ESTs

FIGURE 6

Primary Key	fold downregulated of Tumor	Accession	Unigene CLUSTER	Unigene Descriptor
2348	>10	M15556	Hs.7592	Adipose B fructose-bisphosphate
6463	>10	X93008	Hs.74126	H.sapiens mRNA for I-1P (I-BAPD) protein
42139	>10	T73335	Hs.03194	APOLIPOPROTEIN A-I PRECURSOR
4544	>10	U48955	Hs.76950	H.sapiens mRNA for myosin light chain kinase
1563	>10	K27655	Hs.59512	COMPLEMENT C3 PRECURSOR
2425	>10	M19828	Hs.585	Apolipoprotein B (including Aqg3 antigen)
6659	>10	A3002351	Hs.50587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z33888	Hs.21492	ESTs
17510	>10	A4151402	Hs.46531	H.sapiens mRNA for GCAP-II/unguanylin precursor
7006	>10	Z70255	Hs.32366	ESTs
1304	>10	H34310	Hs.65424	EST - HQ4310A14590
5980	>10	G44559	Hs.12173	Tetranectin (extracellular matrix protein)
41897	>10	T47059	Hs.02173	Cytidine P450 subfamily XM (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	V94427	Hs.3507	ESTs Weakly similar to SODIUMPOTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.65522	Guanidino S-transferase A2
6001	>10	X69727	Hs.69552	Guanidino S-transferase A2
1750	>10	L10855	Hs.69485	Carbonic anhydrase IV
15130	>10	U77643	Hs.95555	Homo sapiens K12 protein precursor mRNA complete cds
12467	>10	AA402656	Hs.25264	ESTs
41146	>10	R08964	Hs.25264	EST - RC_R08964_3
31652	>10	N73958	Hs.50404	Human chemokine (TECK) mRNA complete cds
4605	>10	U51010	Hs.143289	H.sapiens mRNA for metalloprotein isoform 1R
28359	>10	AA609133	Hs.58115	EST - U51010
24066	>10	W32506	Hs.111676	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.00552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R46732	Hs.11006	ESTs
33568	>10	T28248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage gated 1 beta (Liddle syndrome)
26707	>10	N64436	Hs.20813	ESTs
27108	>10	AA404397	Hs.59414	ESTs Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA403332	Hs.21701	APOLIPOPROTEIN A-I PRECURSOR
42059	>10	T61654	Hs.95194	APOLIPOPROTEIN A-I PRECURSOR
25468	>10	AA075072	Hs.1477	Insulin-like growth factor binding protein 6
28910	>10	AA303081	Hs.76253	Insulin-like growth factor binding protein 6

FIGURE 6 (CONT.)

18936	AA059473	Hs.60783	ESTs	
>10		Hs.26855	ESTs	
41766	T03735	Hs.26855	ESTs	
>10	AA234634	Hs.76722	Endoglin (NFI-IL6-beta protein mRNA complete cds	
7754	X72012	Hs.75962	Endoglin (Oiler-Reuda-Wieber syndrome 1)	
6122	M59286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
2048	T18981	Hs.6725	ESTs	
23013	H30270	Hs.32593	ESTs	
19537	U50390	EST - U50390	ESTs	
4594	AA433552	Hs.95344	ESTs	
>10	AA464594	Hs.63382	ESTs	
37410	AA400606	Hs.144344	EST	
>10	AA438990	Hs.135268	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]	
37013	AA621553	Hs.112598	ESTs	
35247	AA452599	Hs.105990	ESTs	
>10	T68878	Hs.76996	Carboxylesterase 2 (liver)	
42110	AA128597	Hs.18953	Homo sapiens GMP-specific phosphodiesterase (PDE3A2) mRNA complete cds	
10955	U67733	Hs.3531	Human cGMP-stimulated 3'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
4916	N54950	Hs.81454	H.sapiens KHK mRNA for ketohexokinase clone pHHK3a	
40737	N45300	Hs.110647	Meis1 (mouse) homolog	
33403	AA233369	Hs.381	ESTs	
>10	F09748	Hs.7974	ESTs	
18784	N49281	EST - RC_N49281	ESTs	
40652	Hs.79396	84 KD AUTOANTIGEN D1	ESTs	
>10	X54162	Hs.30892	ESTs	
33041	AA350589	Hs.7243	ESTs	
>10	N70068	Hs.105805	ESTs	
20866	H11489	Hs.76254	ESTs	
>10	AA426330	Hs.80455	Human apM1 mRNA for GS3109 (novel adipose specific collagen-like factor) complete cds	
27387	H14914	Hs.65892	Human microfilament-associated glycoprotein-2 MAGP-2 mRNA complete cds	
33758	U37233	Hs.76892	Complement component 4A	
4319	M53915	Hs.44594	EST	
2866	N38075	Hs.6985	ESTs	
>10	R40169	Hs.48778	ESTs	
30332	AA521200	Hs.7644	HISTONE H1D	
41344	X57129	Hs.100251	ESTs	
28271	H05454	Hs.9515	Human 20-3a myosin light chain (MLC-2) mRNA complete cds	
5834	J02854	Hs.107384	ESTs	
19046	H27910	Hs.33094	Solute carrier family 2 (facilitated glucose transporter) member 5	
1429	N26385	Hs.77423	Stromal cell-derived factor 1	
19491	L38033	Hs.35186	ESTs	
25992	R99909			
2041				
>10				
22855				

FIGURE 6 (CONT.)

11624	>10	AA243654	Hs.17598	ESTs	
12512	>10	AA405199	Hs.20733	ESTs	
41443	>10	R45577	Hs.10883	ESTs	
5055	>10	U77160	Hs.50002	Human mRNA for EBI1 ligand chemokine complete cds	
6038	>10	X65945	Hs.748	Basic fibroblast growth factor (bFGF) receptor (shorter form)	
42330	>10	W72859	Hs.74569	ESTs Weakly similar to SYNAPTOSOMAL 2 [H.sapiens]	
827	>10	D78433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
650	>10	D78014	Hs.74568	Human mRNA for dihydropyrimidine related protein-3 complete cds	
37350	>10	AA452606	Hs.99289	EST	
37488	>10	AA455178	Hs.95397	ESTs	
36845	>10	AA431797	Hs.98763	EST	
39999	>10	AA609907	EST - RC_AA609907		
38191	>10	AA487895	Hs.17311	ESTs	
5944	>10	N57464	Hs.74570	Human mRNA for KIAA0146 gene partial cds	
8139	>10	AA341723	Hs.107374	ESTs	
41522	>10	R53906	Hs.75092	N-CHIMAERIN	
30090	>10	AA452503	Hs.111301	Matrix metalloproteinase 2 (gelatinase A 72kD gelatinase 72kD type IV collagenase)	
41175	>10	R05241	EST - RC_R05241		
36947	>10	AA437388	Hs.115726	ESTs	
4175	>10	U25953	Hs.76110	Pigment epithelium-derived factor	
35421	>10	AA365686	Hs.97659	EST	
4358	>10	U39457	Hs.230	Xanthine dehydrogenase	
35463	>10	AA400272	Hs.97758	EST	
7028	>10	Z60345	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain	
34525	>10	AA292238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds	
20179	>10	N24879	Hs.9693	ESTs	
38905	>10	AA435901	Hs.56874	ESTs Weakly similar to p20 protein [L.novaeigues]	
24447	>10	W63121	Hs.23841	Human mRNA for KIAA0355 gene complete cds	
10247	>10	R74396	Hs.105924	ESTs	
3616	>10	U02388	Hs.101	Leukodien B4 omega hydroxylase (cytochrome P450 subfamily IVF)	
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR	
15842	>10	AA055163	Hs.57975	Homo sapiens mRNA for cardiac caldesmon complete cds	
16736	>10	AA045306	Hs.42596	ESTs	
22665	>10	R85680	Hs.33455	ESTs	
5248	>10	U86358	Hs.50404	Human chemokine (TECK) mRNA complete cds	
7510	>10	AA136353	Hs.39022	ESTs	
34683	>10	AA284920	Hs.13716	ESTs	
19686	>10	H89980	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [M.musculus]	
9959	>10	N75215	Hs.43148	ESTs	
39135	>10	AA486185	Hs.125176	ESTs	

FIGURE 6 (CONT.)

36702	>10	AA434108	Hs.101393	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
36783	>10	M95487	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
38783	>10	AA435905	Hs.112086	EST
4876	>10	U60061	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R06866	Hs.76487	ESTs
15925	>10	Y13492	Hs.78483	Homo sapiens mRNA for smoothelin
12944	>10	AA429258	Hs.8769	ESTs
9317	>10	H17865	Hs.40888	Human mRNA for KIAA0278 gene partial cds
19331	>10	U74392	Hs.23213	ESTs
5032	>10	U74392	Hs.90357	Homo sapiens telomeric repeat binding factor (TRF1) mRNA complete cds
34239	>10	W31906	Hs.32246	ESTs
32692	>10	X99066	Hs.116428	ESTs
6432	>10	AA443311	Hs.94413	Transient receptor potential channel 1
37001	>10	U52101	Hs.98998	ESTs
4630	>10	H27852	Hs.9959	Human YMP mRNA complete cds
19489	>10	T17215	Hs.28137	ESTs
23028	>10	T17215	Hs.6952	ESTs
35359	>10	AA398061	Hs.112961	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H. sapiens]
4685	>10	U82969	Hs.80296	BRAIN SPECIFIC POLYPEPTIDE PEP-19
26030	>10	AA239984	Hs.87469	ESTs
41348	>10	R40395	Hs.112125	Lactithin-cholesterol acyltransferase
14494	>10	U43916	Hs.25532	ESTs Weakly similar to PNG gene [H. sapiens]
4453	>10	Z14111	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	AA402933	Hs.107940	ESTs
35637	>10	H95687	Hs.26263	ESTs
40392	>10	H19204	Hs.106980	ESTs
19366	>10	H19204	Hs.133466	ESTs
5184	>10	B82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
1595	>10	K03207	Hs.103972	Salivary proline-rich protein
15574	>10	W83778	Hs.26216	ESTs
8965	>10	C00125	Hs.24332	ESTs Weakly similar to deoxyribose-phosphate aldolase [C. elegans]
33995	>10	AA182845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds
7949	>10	AA283620	Hs.34956	ESTs
11970	>10	AA252191	Hs.25199	Homo sapiens PAC clone DJ130H16 from Zdq 2.1-qlar
7354	>10	AA092348	Hs.7958	ESTs
35151	>10	AA413011	Hs.96744	ESTs
42736	>10	T72491	Hs.73949	Apolipoprotein C-III
289	>10	D16480	Hs.75890	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase (trifunctional protein) alpha subunit
41379	>10	R42233	Hs.106487	Homo sapiens mRNA for KIAA0673 protein partial cds

FIGURE 6 (CONT.)

34764	>10	A2287870	Hs.880	Lymphotoxin-beta
24615	>10	Z38289	Hs.12701	ESTs
18652	>10	F03111	Hs.22505	ESTs
37815	>10	A449952	Hs.97999	ESTs
9034	>10	C01833	Hs.29759	ESTs Weakly similar to IIII ALL SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
34805	>10	A231622	Hs.97290	EST
12246	>10	A3448198	Hs.14529	Homo sapiens mRNA for GABA-BR1a (GAB1a) receptor
47153	>10	177729	Hs.69890	Pyruvate carboxylase
27110	>10	A404484	Hs.84112	CTP synthetase
28831	>10	D59722	Hs.92324	ESTs
6333	>10	X62494	Hs.2653	Fibulin 2
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
27257	>10	AA18001	Hs.46146	ESTs Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]
3631	>10	U03060	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
4752	>10	U59532	Hs.3847	Glycoprotein Ib (platelet) beta polypeptide
3766	>10	U09579	Hs.74984	CYCLIN-DEPENDENT KINASE INHIBITOR 1
4310	>10	U37055	Hs.75034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs
5920	>10	X06256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
16720	>10	AA044732	Hs.77208	ESTs
25336	>10	AA063405	Hs.101404	ESTs
2547	>10	M29809	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 59/58kD isoform 1
9795	>10	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
5205	>10	U63978	Hs.67946	Human clone HM16 monocyte inhibitory receptor precursor mRNA complete cds
9377	>10	H12574	Hs.9396	ESTs
41960	>10	T33511	Hs.4844	ESTs
21911	>10	R43960	Hs.26320	ESTs
16225	>10	AA071305	Hs.10029	Calhepsin C
15071	>10	AA071426	Hs.40893	ESTs
28335	>10	H69239	Hs.39122	ESTs
34966	>10	AA344666	Hs.1285	Complement component 8 gamma polypeptide
21076	>10	N99976	Hs.8016	ESTs
4402	>10	U41516	Hs.74602	AQUAPORIN-CHIP
20423	>10	N49308	Hs.104938	ESTs
16575	>10	AA031948	Hs.67548	ESTs
28264	>10	AA521080	Hs.46785	ESTs
9003	>10	C00808	Hs.107862	ESTs
5632	>10	X15357	EST - X15357	
20852	>10	N69540	Hs.17713	ESTs
34585	>10	AA261302	Hs.40735	ESTs

FIGURE 6 (CONT.)

33650	>10	Z39507	Hs.62248	ESTs
8504	>10	AF002255	Hs.85180	Human sapiens killer cell receptor (KIR103) mRNA allele: ASD1 complete cds
3307	>10	M69509	Hs.89578	BASIC TRANSCRIPTION FACTOR 62 KO SUBUNIT
39200	>10	AA671246	Hs.112956	EST
24712	>10	Z39552	Hs.27457	ESTs
2199	>10	LA9169	Hs.75678	Human GOS3 mRNA complete cds
38942	>10	AA69546	Hs.94970	Human mRNA for KIA0306 gene partial cds
41628	>10	R70212	Hs.79530	Immunoglobulin-associated alpha
6834	>10	Z18954	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)
40562	>10	N33212	Hs.107197	ESTs
37333	>10	AA432155	Hs.75122	TRANSFORMING PROTEIN RHOB
3992	>10	U19713	Hs.76384	Allograft inflammatory factor 1
39734	>10	AA608792	Hs.112591	EST
37836	>10	AA470135	Hs.112238	ESTs
10000	>10	N76674	Hs.7915	ESTs
30668	>10	N51105	Hs.111223	ESTs
17829	>10	AA131919	Hs.69009	ESTs
39260	>10	AA423970	Hs.98378	ESTs
24122	>10	W46947	Hs.4188	ESTs
1096	>10	HG2706-	EST - HG2705-HT261	
12389	>10	AA398633	Hs.24672	ESTs
26025	>10	AA235874	Hs.80686	PUTATIVE DNA BINDING PROTEIN A20
41104	>10	R01398	EST - RC_R01398	
33596	>10	W93015	Hs.73166	Treacher Collins syndrome susceptibility protein
26379	>10	AA088933	Hs.111841	Human adenovyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds
17307	>10	AA119030	Hs.72447	ESTs
39838	>10	AA438163	Hs.95851	Human sapiens Pg12 (Pg12) mRNA complete cds
15524	>10	HQ5966	Hs.83466	Human sapiens clone 23579 mRNA sequence
21934	>10	R44449	Hs.48778	ESTs
32456	>10	T15829	Hs.69254	ESTs
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermonospora curvula]
2907	>10	M58210	Hs.87428	Leishman gamma 1 (formerly LMB2)
34183	>10	AA322251	Hs.126330	ESTs
14534	>10	AA671414	Hs.110003	Human sapiens transmembrane protein mRNA complete cds
39752	>10	AA698362	Hs.112003	EST
5294	>10	U00065	Hs.79351	Human hsp P-domain K+ channel TWIK-1 mRNA complete cds
84	>10	AF001359	EST - AF001359_1	
4866	>10	U65093	Hs.82071	Human magi-related gene 1 (mg1) mRNA complete cds
13974	>10	AA478259	RZ1107	ESTs
26151	>10	AA230535	Hs.105509	ESTs

FIGURE 6 (CONT.)

5038	>10	X62535	Hs.74044	Dialkylglycerol kinase alpha (R0KD)
17717	>10	AA136541	Hs.71647	EST
12404	>10	AA400232	Hs.23786	ESTs
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR
26620	10	AA260413	Hs.89843	Spizzen focus forming virus (SFFV) proviral integration oncogene sp1
37675	10	AA460377	Hs.98916	ESTs
41827	10	T15445	Hs.99491	H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans
82	10	AF000669	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
203	10	D12620	Hs.105242	CYTCHROME P450 1F3
24159	10	W57952	Hs.21289	ESTs
5302	10	U99543	Hs.79941	Human butyrophilin (BTFL1) mRNA complete cds
2219	10	L76670	Hs.105910	Homo sapiens ricat7 mRNA complete cds
24392	10	W69568	Hs.95659	Homo sapiens glycogenin-2, gamma (glycogenin-2) mRNA complete cds
36159	10	AA419270	Hs.82813	Codon-eliminating factor 1 (M-CSE)
29251	10	AA504512	Hs.76852	ESTs Weakly similar to ZK792.1 [C.elegans]
37692	10	AA459568	Hs.95898	ESTs
38619	8	F10640	Hs.12354	ESTs
8240	8	AA397641	Hs.108879	ESTs
19687	8	AA110132	Hs.22971	ESTs
37590	8	AA455474	Hs.105330	ESTs
42850	8	W92272	Hs.25691	Homo sapiens zinc-finger helixase (ZFH1) mRNA complete cds
9911	8	C01384	Hs.108323	Homo sapiens gene 24518 mRNA sequence
3480	8	S77763	Hs.75843	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
36951	8	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE [H.sapiens]
3478	8	T59592	Hs.104005	Var. 2 oncogene
42034	8	T59281	Hs.110440	Human metallothionein (MT)-F gene
11845	8	AA256984	Hs.10839	ESTs Weakly similar to unknown [S.cerevisiae]
19317	8	H17376	Hs.11615	ESTs Weakly similar to dual specificity phosphatase [H.sapiens]
42365	8	W62733	Hs.108970	ESTs
11425	8	AA332357	Hs.25511	Homo sapiens mRNA for Hic-5 partial cds
13310	8	W19098	Hs.7921	ESTs
35601	8	AA431337	Hs.56017	ESTs
13459	8	AA453058	Hs.7301	ESTs
17514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1
5698	8	X65044	Hs.75963	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2
33569	8	W63074	Hs.58342	ESTs
5801	8	X54448	Hs.3116	H.sapiens mRNA for 2.19 gene
11129	8	AA119673	Hs.15970	ESTs
31987	8	N94551	Hs.55060	ESTs
40438	8	N21684	Hs.80500	Human mRNA for KIAA0061 gene partial cds

FIGURE 6 (CONT.)

34471	8	AA258843	Hs.111376	ESTs	
25330	8	AA098834	Hs.83428	Nucleic factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	
39471	7	D60265	Hs.107684	ESTs	
25100	7	AA018426	Hs.103343	EST	
15515	7	Y09858	Hs.92577	Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34) hypothetical protein E	
18097	7	H08171	Hs.30842	ESTs	
35553	7	AA398962	Hs.07689	ESTs	
38622	7	AA435978	Hs.98852	EST	
35530	7	AA400893	Hs.41717	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDE1A3A) mRNA complete cds	
1979	7	L29339	Hs.19147	Human Raf guanine nucleotide dissociation stimulator mRNA, partial cds	
1879	7	Hs.1954	Hs.16185	Solute carrier family 5 (sodium/glucose cotransporter) member 1	
25178	7	AA251153	Hs.27910	Human sapient centrosomal Nck2-associated protein 1 (C-NAP1) mRNA complete cds	
38428	7	AA427605	Hs.98551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds	
26333	7	AA256075	Hs.82280	Human sapient regulator of G protein signaling 10 mRNA complete cds	
40387	7	H95460	Hs.108873	ESTs	
27235	7	AA417037	Hs.67805	ESTs	
20083	7	H96879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH-FACTOR PRECURSOR [Mus musculus]	
21223	7	R33245	Hs.23076	ESTs	
21591	7	R08175	Hs.110130	ESTs	
13405	7	AA450118	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]	
34845	7	AA283420	Hs.85464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]	
15059	7	U53831	Hs.85280	Human Interleukin regulatory factor 7 (lunifit7) mRNA complete cds	
1945	7	L25878	Hs.89649	Erythroid hydrolase 1 (microsomal xenobiotic)	
42648	7	W62150	Hs.79310	Human GAP Sh3 binding protein mRNA complete cds	
20041	7	H97012	Hs.11050	ESTs Weakly similar to L3004.7 gene product [S. cerevisiae]	
7053	9	Z54721	Hs.75792	Hemoglobin alpha 1	
23843	8	T52561	Hs.110422	ESTs	
25815	8	AA146889	Hs.95200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.novgicus]	
8473	8	AA437346	Hs.2987	SHB adaptor protein (a Src homology 2 protein)	
34518	8	AA282143	Hs.58094	H.sapiens mRNA for melanoma growth regulatory protein MIA	
11074	8	AA148883	Hs.29068	ESTs	
17533	8	AA127068	Hs.71057	EST	
28873	8	F54014	Hs.65996	ESTs	
17042	8	AA070397	Hs.4407397	EST - RC_AA070397	
15246	8	W01084	Hs.84528	ESTs	
2247	8	M10331	Hs.119802	VON WILLEBRAND FACTOR PRECURSOR	
33810	8	NS3419	Hs.47566	ESTs	
13346	8	AA446267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA SUBUNIT [M.musculus]	
1789	8	L13259	Hs.938	Solute carrier family 17 (sodium phosphate) member 2	
16627	8	AA035779	Hs.61826	Human sapient clone 23923 mRNA sequence	

FIGURE 6 (CONT.)

27103	5	AA404282	Hs.63481	ESTs Weekly similar to kynurenine/alpha-aminoadipate aminotransferase [R.norvegicus]
12831	5	AA412283	Hs.27258	ESTs
11599	5	AA242829	Hs.7508	ESTs
9010	5	C01360	Hs.67364	Homo sapiens clone 23504 mRNA sequence
4680	5	U53225	Hs.75263	Sorting nexin 1
5244	5	U85692	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds
5343	5	AA284403	Hs.74750	Homo sapiens mRNA for KIA00554 protein partial cds
27617	5	AA446114	Hs.55409	ESTs
39480	5	D60419	Hs.81915	STATHMIN
37529	5	AA456112	Hs.99410	ESTs
11658	5	AA262308	Hs.100385	ESTs
37294	5	AA450127	Hs.110571	ESTs Highly similar to MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118 [Mus musculus]
23201	5	T40552	Hs.8279	ESTs
28767	5	D45606	Hs.63792	Surfactant pulmonary-associated protein D
3151	4	M83952	Hs.53155	Properdin P factor complement
29196	4	H24456	Hs.65053	Homo sapiens clone 24440 mRNA sequence
12863	4	AA425782	Hs.27573	ESTs
42466	4	W65410	Hs.106557	Calbindin 2 (28kD calininin)
23571	4	T80528	Hs.108169	ESTs
12376	4	AA388271	Hs.19610	ESTs
27894	4	AA450319	Hs.48469	ESTs
24635	4	AFFX-	AFFX-HUMGAPDH/M33197_M	
4708	4	U33053	Hs.2499	Human lipid-activated protein kinase PRK1 mRNA complete cds
41844	4	T15833	Hs.100227	EST
20111	4	N21380	Hs.25497	H.sapiens mRNA for FOX protein
8316	4	AA410529	Hs.30732	ESTs
39794	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D30081	Hs.85987	Thrombosane A2 receptor
35027	4	AA349966	Hs.95637	ESTs
14158	4	AA480182	Hs.118598	ESTs
41950	4	T31137	Hs.7987	ESTs
34350	4	AA251547	Hs.104358	EST
6547	4	X95908	Hs.9598	Human mRNA for KIA0385 gene complete cds
20863	4	N95989	Hs.19167	ESTs
12734	4	AA418200	Hs.5737	ESTs
39497	4	D60154	Hs.56340	ESTs
1500	4	K03474	EST - K03474	
27146	4	AA486231	Hs.100113	Human mRNA for KIA0381 gene partial cds
10763	4	AA057620	Hs.30807	ESTs

FIGURE 6 (CONT.)

17007	4	AA059596	Hs.67317	ESTs	
13322	4	AA454115	Hs.6000	ESTs	
18444	4	AA322646	Hs.60061	ESTs	
27665	3	AA447759	Hs.34724	ESTs	
21382	3	R16906	Hs.89915	PROTEIN KINASE C THETA TYPE	
2032	3	L36816	Hs.75539	Inositol polyphosphate phosphatase-like protein 1 (51C protein)	
9039	3	C22049	Hs.105291	ESTs	
34869	3	AA303078	Hs.94479	Human GT334 protein (GT334) gene mRNA complete cds	
11047	3	AA142949	Hs.22560	ESTs	
19451	3	H23747	Hs.31597	ESTs	
2822	3	M55921	Hs.117946	Naosylglucosaminyltransferase 1	
13929	3	AA478441	Hs.11590	ESTs	
12054	3	AA263948	Hs.11367	ESTs Weakly similar to KIAA0009 [H.sapiens]	
3936	3	U12707	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	
4298	3	U49251	Hs.75571	Homo sapiens protein kinase C-binding protein RACK7 mRNA partial cds	
42904	3	T63954	Hs.9295	ESTs Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parusichopus parvimerens]	
4396	3	U57243	Hs.19320	Sodium/potassium ATPase gamma subunit	
4514	3	U57611	EST - U57611		
20168	3	N24106	Hs.2799	Cartilage linking protein 1	
24281	3	W79773	Hs.18511	ESTs	
19534	3	H44695	Hs.31597	ESTs	
19899	3	AA132366	Hs.8023	Homo sapiens mRNA for SPOF	
6561	3	X97748	EST - X97748		
1436	3	AA457558	Hs.8195	ESTs	
13350	3	AA449297	Hs.8544	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]	
33300	3	AA189639	Hs.95870	ESTs	
34215	3	AA235855	Hs.104252	UTROPHIN	
22069	3	R71593	Hs.29190	ESTs	
20055	3	H69557	Hs.27231	ESTs	
31051	3	N63076	Hs.136746	ESTs	
2493	3	M22519	Hs.77365	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
28913	3	FO1560	Hs.22565	ESTs Highly similar to co-repressor protein [Mus musculus]	
14323	3	AA398575	Hs.12851	ESTs	
34914	3	AA338729	Hs.13096	ESTs	
14236	3	AA495951	Hs.50111	ESTs Weakly similar to The h4237 gene product is related to S.pombe rad21 gene product [H.sapiens]	
24594	3	Z38604	Hs.22555	ESTs Highly similar to OP10D BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos taurus]	
22569	3	R79590	Hs.29674	ESTs	
R52145	3	Hs.25894	ESTs		
22156	3	AA021264	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R. norvegicus]	
16404	3	H69542	Hs.88729	ESTs	
28310	3				

FIGURE 6 (CONT.)

3	M25393	Hs.127610	Aryl-Ceramide A dehydrogenase C-2 to C-3 short chain
2	H73462	Hs.69633	Probable transcription factor PML (alternative products)
2	H10566	Hs.23746	ESTs
2	AA182614	Hs.63377	Human LIM protein MLP mRNA complete cds
2	W73790	Hs.73803	IMMUNOGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
2	M63716	Hs.76983	Nitric oxide synthase 3 (endothelial cell)
2	N73055	Hs.14632	ESTs
2	R67373	Hs.75429	ESTs
2	R63695	Hs.1432	Protein kinase C substrate 80K-H
2	N73988	Hs.37477	ESTs Weakly similar to No definition line found [C.elegans]
2	X62466	Hs.105338	CDW52 antigen (CAMPATH-1 antigen)
2	R46869	Hs.5260	ESTs Weakly similar to C0863.3 [C.elegans]
2	AA083316	EST - RC_AA083316	
2	AA44267	Hs.24912	Homo sapiens bicucullin-D (BICD) mRNA complete cds
2	N45221	EST - RC_N45221	
2	N74336	Hs.63260	Phosphodiesterase 6A cGMP-specific rod alpha
2	HG1804-	Hs.91681	ESTs
2	AA401462	Hs.32060	EST - HG1804-HT1829
2	N70168	Hs.26996	ESTs
2	N83764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]
2	AA215637	Hs.104186	ESTs
2	U79288	Hs.85053	Homo sapiens clone 24440 mRNA sequence
2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
2	H17509	Hs.22482	ESTs
2	R40442	Hs.75652	Glutathione S-transferase M5
2	HG1019-	EST - HG1019-HT1019	
2	NS3485	Hs.54960	ESTs
2	AA281769	Hs.7214	Human HpaST (HPAST) mRNA complete cds
2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isozyme dehydrogenase gamma subunit mRNA alternatively spliced partial cds
2	H09751	Hs.117819	ESTs
2	AA176446	Hs.10024	ESTs
2	X81504	Hs.64904	Transcription factor COUP 2 (a.k.a. ARP1)
2	AA018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3
2	W23709	Hs.109047	ESTs
2	AA251230	Hs.112272	ESTs
2	AA447988	Hs.7765	ESTs
2	T47601	Hs.138805	ESTs
2	AA428889	Hs.68882	Acrosin
2	J03071	Hs.115352	Growth hormone 1

FIGURE 6 (CONT.)

24819	2	Z40923	Hs.24812	ESTs	
6532	2	X95325	Hs.89491	DNA-BINDING PROTEIN A	
27085	2	AA402495	Hs.77978	ESTs	
20487	2	N52322	Hs.19578	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.82294	Human RGP3 mRNA complete cds	
13375	2	AA449716	Hs.5723	ESTs	
13988	2	AA480045	Hs.7934	ESTs	
22308	2	R55905	Hs.100530	ESTs	
23167	2	T33164	Hs.12940	Homo sapiens germline mRNA sequence	
11320	2	AA213987	Hs.22222	ESTs	
24608	2	Z38898	Hs.25048	ESTs	
13163	2	AA437225	Hs.22410	ESTs	
1139	2	HG3227-	EST - HG3227-HT3404		
35572	2	AA401489	EST - RC_AA401489		
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
30963	2	N59373	Hs.26812	ESTs	
19164	2	AA007509	Hs.75395	Human mRNA for TP6D complete cds	
2174	2	L42611	Hs.117258	VERBATIN TYPE II CYTOSKELETAL BD	
38958	2	AA609707	Hs.112751	ESTs	
37019	2	AA478162	Hs.104685	ESTs	
28305	2	D81123	Hs.57475	ESTs	
3743	2	U09117	Hs.80775	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32659	ESTs	
8416	2	AA428531	EST - AA428531		
17699	2	AA128528	EST - RC_AA128528		
19324	2	H18529	Hs.121515	ESTs	
7398	2	AA174185	Hs.3254	Human sapiens ectin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25395	2	AA050099	Hs.109727	ESTs	
41776	2	AA408020	Hs.11809	ESTs	
29497	2	H85120	Hs.80881	N-ACETYL-LACTOSAMINE SYNTHASE	
10197	2	R84199	Hs.50785	Human sapiens vesicle trafficking protein sec22b mRNA complete cds	
19468	2	AA028703	Hs.25604	ESTs	
30799	2	H27675	Hs.35574	ESTs	
9638	2	N83143	Hs.04001	ESTs	
27195	2	L07352	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds	
17438	2	AA411473	Hs.60311	ESTs	
24932	2	AA115508	Hs.2780	Jun D proto-oncogene	
10944	2	AFFX-	AFFX-HSAC07X00351 JM		
	2	AA125989	Hs.34769	ESTs Weakly similar to F35G12.9 [C.elegans]	

FIGURE 6 (CONT.)

42324	2	T08159	Hs.142702	ESTs	
34755	2	AA287665	Hs.8245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
13675	2	AA450389	Hs.26350	Homo sapiens mRNA for tyrosyl sulfotransferase-2	
13009	2	AA430474	Hs.16466	ESTs	
7403	2	AA094021	Hs.79768	ESTs	
35669	2	AA047707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71526	ESTs	
10713	2	P04866	Hs.21782	ESTs	
8314	2	AA103355	Hs.103651	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	
7990	2	AA231786	Hs.32822	ESTs Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	
42781	2	AF14	AF14-HUMGALP4/493197_M	AF14-HUMGALP4/493197_M	
6693	1	Z30543	Hs.123123	H sapiens mRNA for chloride channel (putative) 2139bp	
35607	1	AA422267	Hs.139475	ESTs Weakly similar to zinc finger protein [H.sapiens]	
9468	1	H45074	Hs.31552	ESTs	
28469	1	H63629	Hs.8217	EST - RC_H22229	
18692	1	P04444	Hs.6217	ESTs	
32005	1	AA386161	Hs.97602	ESTs	
22184	1	RS3320	Hs.102795	ESTs	
28815	1	D6267	Hs.56762	ESTs	
17813	1	AA151450	Hs.97202	ESTs	
24695	1	Z39191	Hs.27262	ESTs Weakly similar to Lph1Tp [S.cerevisiae]	
15611	1	W51743	Hs.35096	ESTs	
15700	1	W73699	Hs.75961	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds	
36770	1	AA435753	EST - RC_AA435753	EST - RC_AA435753	
32400	1	R87178	Hs.110783	ESTs	
10902	1	AA069425	Hs.20573	ESTs	
17593	1	AA129866	EST - RC_AA129866	EST - RC_AA129866	
20296	1	N32118	Hs.107385	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]	
14447	1	AA009045	Hs.11759	ESTs	
12892	1	AA426521	Hs.18528	Homo sapiens mRNA for NA14 protein	
19735	1	H63059	Hs.15548	ESTs	
14471	1	AA009346	Hs.20102	ESTs	
5796	1	X55019	Hs.99875	Cholinergic receptor nicotinic delta polypeptide	
18441	1	AA323508	Hs.77480	ESTs	
10164	1	RS4743	Hs.19400	ESTs Weakly similar to MITOCH MAOZ PROTEIN [S.cerevisiae]	
8830	1	AB002319	Hs.89653	Human mRNA for KIAA0321 gene partial cds	
8982	1	AA477891	Hs.104476	ESTs	
35620	1	AA402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	AA359993	Hs.97662	EST	

FIGURE 6 (CONT.)

105901	1	AA112307	Hs.25224	ESTs	
10546	1	H37501	Hs.32706	ESTs	
30332	1	N5978	Hs.52384	ESTs	
30687	1	AA205507	Hs.11551	ESTs	
37696	1	AA477463	Hs.70169	Ribosomal protein, S28	
41552	1	R5632	Hs.10163	Human mRNA for KIAA0296 gene complete cds	
11457	1	AA234059	Hs.14353	ESTs	
8215	1	AA35973	Hs.54344	ESTs Weakly similar to No definition line found [C.elegans]	
15305	1	V22356	Hs.7222	Homo sapiens clone 24800 mRNA sequence	
9534	1	M92289	Hs.22554	Homo box B5 (2.1 protein)	
9159	1	D31483	Hs.30062	Homo sapiens clone 23565 unknown mRNA partial cds	
42718	1	T65444	Hs.110095	ESTs	
15526	1	V28790	Hs.8124	ESTs	
17790	1	AA150162	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN (K02D10.1 IN CHROMOSOME III [C.elegans])	
9777	1	M97888	Hs.59546	GRANULIN H PRECURSOR	
15373	1	V28376	Hs.74593	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
12075	1	AA284352	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]	
15391	1	V28651	Hs.15561	ESTs	
15391	1	AA427537	Hs.32419	ESTs	
12505	1	H24085	Hs.25443	ESTs	
39820	1	AA435538	Hs.7985	ESTs	
13109	1	V73069	Hs.12600	ESTs	
24249	1	W73069	Hs.12600	ESTs	
16514	1	AA027946	Hs.44608	ESTs	
16757	1	AA046550	Hs.40342	ESTs	
15381	1	V25456	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]	
11660	1	AA252762	Hs.31235	ESTs	
22859	1	T18510	Hs.6624	ESTs	
24490	1	Z38153	Hs.26921	ESTs	
24398	1	W87280	Hs.124800	ESTs	
22565	1	R77631	Hs.29126	ESTs	
15358	1	W26105	Hs.5561	ESTs	
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]	
22272	1	R59922	Hs.26550	ESTs	
16434	1	AA024494	Hs.61199	ESTs	
22692	1	R88711	Hs.34183	ESTs	
38830	1	AA608189	Hs.116415	ESTs	
42547	1	V73946	EST - RC_W73946	EST - RC_W73946	
34885	1	AA302631	Hs.57732	Homo sapiens p38beta MAP kinase mRNA complete cds	
18445	1	AA232646	Hs.57066	ESTs	
18070	1	AA180352	Hs.72733	ESTs	

FIGURE 6 (CONT.)

23923 1 T96407 Hs.7812 ESTs

FIGURE 7

Primary Key	fold downregulated of Tumor vs	Accession	UniGene CLUSTER	UniGene Descriptor
2348	>10	M15656	Hs.75592	Adipose B fructose-bisphosphate
6463	>10	X90808	Hs.74126	H.sapiens mRNA for h-1p (h-RBP) protein
42139	>10	T73335	Hs.93194	APOLIPROTEIN A-I PRECURSOR
4544	>10	A06559	Hs.78550	H.sapiens mRNA for myoath light chain kinase
1553	>10	K02765	Hs.59512	COMPLEMENT C3 PRECURSOR
2426	>10	M19422	Hs.305	Apolipoprotein B (including ApoB) antigen
8659	>10	AB02351	Hs.10587	Human mRNA for KIAA0353 gene partial cds
24572	>10	Z39689	Hs.24192	ESTs
17810	>10	AA151402	Hs.46531	ESTs
7006	>10	Z70295	Hs.32966	H.sapiens mRNA for GCAP-1/uroguanylin precursor
1324	>10	HG4310-	EST - HG4310-HT4580	
5980	>10	X04559	Hs.55424	Tetranectin (plasminogen-binding protein)
41987	>10	T47089	Hs.121713	Cytochrome P450 subfamily XXI (steroid 21-hydroxylase congenital adrenal hyperplasia)
24461	>10	W94427	Hs.3807	ESTs Weakly similar to SODIUM/POTASSIUM-TRANSPORTING ATPASE GAMMA CHAIN [Mus musculus]
2372	>10	M16594	Hs.89552	Glutathione S-transferase A2
6001	>10	X65727	Hs.89552	Glutathione S-transferase A2
1750	>10	L10955	Hs.89495	Carbonic anhydrase IV
15130	>10	U77543	Hs.59555	Homo sapiens K12 protein precursor mRNA complete cds
12457	>10	AA402556	Hs.28254	ESTs
41148	>10	R06584	EST - RC_R06594_s	
31652	>10	N73558	Hs.50404	Human chemokine (TECK) mRNA complete cds
23483	>10	T68973	Hs.143289	H.sapiens mRNA for metallothionein isoform 1R
4605	>10	U51010	EST - U51010	
28359	>10	AA609133	Hs.58115	ESTs
24956	>10	W32506	Hs.111576	ESTs Weakly similar to HEAT SHOCK 27 KD PROTEIN [H.sapiens]
33282	>10	W73194	Hs.80552	ESTs
12084	>10	AA284767	Hs.21910	ESTs
41473	>10	R48732	Hs.11006	ESTs
32568	>10	T35248	Hs.143113	Human pancreatic lipase related protein 2 (PLRP2) mRNA complete cds
6413	>10	X87159	Hs.37129	Sodium channel nonvoltage-gated 1 beta (Liddle syndrome)
20707	>10	N94436	Hs.20013	ESTs
27108	>10	AA040397	Hs.58414	ESTs Highly similar to ENDOTHelial ACTIN-BINDING PROTEIN [Homo sapiens]
12477	>10	AA040392	Hs.21701	ESTs
42959	>10	T81654	Hs.93194	APOLIPROTEIN A-I PRECURSOR
25468	>10	AA075072	Hs.1477	Insulin-like growth factor binding protein 6
26910	>10	AA303081	Hs.78253	ESTs

FIGURE 7 (CONT.)

16938	>10	A4059473	Hs.65783	ESTs	
41788	>10	T03735	Hs.25885	ESTs	
7754	>10	A4234634	Hs.76722	Human NF-IL6-beta protein mRNA complete cds	
6122	>10	X72012	Hs.75982	Endoglin (Oiler-Rendu-Weber syndrome 1)	
2848	>10	M58286	Hs.159	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR	
23013	>10	T16881	Hs.67255	ESTs	
19537	>10	H30270	Hs.32583	ESTs	
4594	>10	U50360	Hs.02070	EST - U50360	
37410	>10	A4453652	Hs.93344	ESTs	
27969	>10	A4464594	Hs.63382	ESTs	
35497	>10	A4407606	Hs.143344	EST	
37013	>10	A4443690	Hs.13858	ESTs Highly similar to ZINC FINGER PROTEIN HF.12 (Homo sapiens)	
39247	>10	A4424553	Hs.12358	ESTs	
13471	>10	A4452538	Hs.10860	ESTs	
42110	>10	T58870	Hs.76888	Carboxylesterase 2 (liver)	
10565	>10	A4128987	Hs.18853	Homo sapiens cAMP-specific phosphodiesterase (PDE5A2) mRNA complete cds	
4716	>10	X17333	Hs.3531	Human cAMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
45737	>10	M51560	Hs.3344	Human cAMP-stimulated 3',5'-cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA complete cds	
30237	>10	M51560	Hs.10347	Hs.10347	
11432	>10	A4233369	Hs.351	ESTs	
18784	>10	F09245	Hs.7974	EST - RQ_140281	
40662	>10	N49281	Hs.79386	64 KD AUTOANTIGEN D1	
5773	>10	X54162	Hs.50862	ESTs	
35041	>10	A4350586	Hs.7243	ESTs	
20898	>10	N70068	Hs.7243	ESTs	
39729	>10	H11488	Hs.105930	ESTs	
37356	>10	A4263330	Hs.76284	ESTs	
39756	>10	H15814	Hs.60465	Human apM1 mRNA for GSI108 (novel adipose specific collagen-like factor) complete cds	
4319	>10	U37263	Hs.55582	Human microfilament-associated glycoprotein-2 MAGP-2 mRNA complete cds	
2866	>10	M59815	Hs.76582	Complement component 4A	
30332	>10	N35075	Hs.44934	EST	
39729	>10	R40189	Hs.6995	ESTs	
28271	>10	A4821200	Hs.48778	ESTs	
5834	>10	X57129	Hs.7644	HISTONE H1D	
19048	>10	H05464	Hs.100251	ESTs	
1429	>10	J02854	Hs.9615	Human 20-kDa myosin light chain (MLC-2) mRNA complete cds	
19491	>10	H27910	Hs.107384	ESTs	
23692	>10	N26396	Hs.33384	Solute carrier family 2 (facilitated glucose transporter) member 5	
2041	>10	L36033	Hs.77423	Stromal cell-derived factor 1	
22955	>10	R99909	Hs.36186	ESTs	

FIGURE 7 (CONT.)

11624	A0243654	Hs.17998	ESTs	
12512	A4405199	Hs.20733	ESTs	
41443	R45577	Hs.10883	ESTs	
5055	U77180	Hs.50002	Human mRNA for EBI-1 ligand chemokine complete cds	
6038	X68945	Hs.7448	Basic fibroblast growth factor (bFGF) receptor (shorter form)	
42530	W72659	Hs.74669	ESTs Weakly similar to SYNAPTOTREVIN 2 [H.sapiens]	
827	D67433	Hs.84753	Human mRNA for KIAA0246 gene partial cds	
650	D78014	Hs.74566	Human mRNA for dihydropyrimidinase related protein-3 complete cds	
37350	A4452506	Hs.99289	EST	
37488	A4455178	Hs.99397	ESTs	
38646	A4431797	Hs.98763	EST	
38999	A4609807		EST - RC_A4609807	
38191	A4487895	Hs.17311	ESTs	
9944	N57464	Hs.74670	Human mRNA for KIAA0146 gene partial cds	
8139	A341723	Hs.107374	ESTs	
41522	R53966	Hs.75092	N-CHIMAERIN	
38090	A4482603	Hs.111301	Matrix metalloproteinase 2 (Gelatinase A 72KD gelatinase 72KD type IV collagenase)	
41175	R09241		EST - RC_R09241	
38947	A4437388	Hs.115726	ESTs	
4175	U29953	Hs.76110	Pigment epithelium-derived factor	
35421	A4395496	Hs.97669	EST	
4358	U39487	Hs.250	Xanthine dehydrogenase	
35453	A4400272	Hs.97758	EST	
7026	Z63345	Hs.127610	Acy-Coenzyme A dehydrogenase C-2 to C-3 short chain	
34625	A282238	Hs.118463	Homo sapiens clone 24519 unknown mRNA partial cds	
20179	N24879	Hs.5993	ESTs	
38805	A4435501	Hs.56874	ESTs Weakly similar to p20 protein [R.novvegicus]	
24447	W93121	Hs.23841	Human mRNA for KIAA0355 gene complete cds	
10247	R74386	Hs.108924	ESTs	
3516	U02388	Hs.101	Leukotriene B4 omega hydroxylase (cyclochrome P450 subfamily IVF)	
18730	F08776	Hs.8008	ESTs	
22529	R73075	Hs.29327	EST	
37520	A4455680	Hs.98405	ESTs	
41122	R05453	Hs.138500	ESTs	
4417	U42031	Hs.7557	Human 54 kDa progesterone receptor-associated immunophilin FKBP54 mRNA partial cds	
9742	M14777	Hs.89552	Glutathione S-transferase A2	
36194	A4421142	Hs.104672	ESTs	
4445	U43653	Hs.3261	Lipin (murine obesity homolog)	
15749	H53728	Hs.36808	ESTs	
15793	H65965	Hs.34554	ESTs	

FIGURE 7 (CONT.)

12713	>10	AA415398	Hs.17778	ESTs
1464	>10	J03474	Hs.3157	SERUM AMYLOID A PROTEIN PRECURSOR
16842	>10	AA059163	Hs.57975	Homo sapiens mRNA for cardiac caldesmon complete cds
34229	>10	AA234383	Hs.3576	ESTs
35563	>10	AA407404	Hs.112087	ESTs
16736	>10	AA043306	Hs.42996	ESTs
33607	>10	W93497	Hs.59486	ESTs
16146	>10	AA005236	Hs.60162	ESTs
22666	>10	R85890	Hs.33455	ESTs
22662	>10	R77493	Hs.29653	EST
22865	>10	T16211	Hs.6326	Homo sapiens clone 23796 and 23825 mRNA sequence
5248	>10	U86558	Hs.50404	Human chemokine (TECK) mRNA complete cds
27008	>10	AA443800	Hs.43125	ESTs
34683	>10	AA136353	Hs.38022	ESTs
7510	>10	AA284920	Hs.13716	ESTs
32485	>10	AA446659	Hs.2563	Tachykinin 2 (substance K neurokinin A neurokinin 2 neurokinin L neurokinin alpha neurokinin gamma)
27633	>10	T16335	Hs.65325	EST
38791	>10	AA609018	Hs.112629	ESTs
32020	>10	N85796	Hs.55181	ESTs
19866	>10	R85890	Hs.12112	ESTs Moderately similar to protein phosphatase 1 binding protein PTG [Musculus]
30748	>10	N82564	Hs.47438	ESTs
6903	>10	AF002246	Hs.21226	Homo sapiens neural cell adhesion molecule (CALL) mRNA complete cds
9595	>10	N75215	Hs.43146	ESTs
38136	>10	AA469185	Hs.125178	ESTs
19845	>10	H59887	Hs.35167	ESTs
1127	>10	HG3117-	EST - HG3117-HT3293	
23637	>10	T85315	Hs.15903	ESTs
18699	>10	AA043349	Hs.62830	ESTs
36702	>10	AA434108	Hs.10193	ESTs Moderately similar to DNAJ PROTEIN HOMOLOG 1 [Homo sapiens]
28930	>10	F02702	Hs.141903	Small inducible cytokine A5 (RANTES)
9226	>10	D62564	Hs.109439	ESTs Highly similar to OSTEOINDUCTIVE FACTOR PRECURSOR [Bos taurus]
3367	>10	M99467	Hs.1915	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
36763	>10	AA435805	Hs.112065	EST
4376	>10	U69051	Hs.2048	Protease serine 2 (trypsin 2)
41149	>10	R05866	Hs.76487	ESTs
22200	>10	R54179	Hs.26100	ESTs
15925	>10	Y13462	Hs.78463	Homo sapiens mRNA for smoothelin
10911	>10	AA113387	Hs.24305	ESTs
3336	>10	N97075	Hs.1944	Human protein tyrosine kinase L-Rort1 (Rort1) mRNA complete cds
31869	>10	N91697	Hs.50552	ESTs

FIGURE 7 (CONT.)

10408	>10	AA007629	Hs.25478	ESTs	
17737	>10	AA143875	Hs.71710	ESTs	
38038	>10	AA006832	Hs.112737	EST	
16266	>10	AA010811	Hs.60416	EST	
32310	>10	VI15378	Hs.72266	ESTs	
16210	>10	AA136306	Hs.68045	ESTs	
24054	>10	VI15580	Hs.15342	ESTs	
23847	>10	T23457	Hs.7120	ESTs	
12344	>10	AA423258	Hs.8769	ESTs	
34172	>10	AA227469	Hs.139717	EST	Human mRNA for KIAA0278 gene partial cds
9317	>10	D87468	Hs.40889	ESTs	
19331	>10	H17985	Hs.23213	ESTs	
21035	>10	N62824	Hs.14898	ESTs	
34208	>10	AA233380	Hs.104249	EST	
5974	>10	X94072	Hs.83968	Integrin beta 2 (antigen CD18 (p85) lymphocyte function-associated antigen 1 macrophage antigen 1 (mac-1) beta subunit)	
5032	>10	U74392	Hs.90357	Homo sapiens isomeric repeat binding factor (TRF1) mRNA complete cds	
41941	>10	T32581	Hs.5478	ESTs	
34239	>10	AA235009	Hs.32246	ESTs	
32952	>10	W31805	Hs.116428	ESTs	
7882	>10	AA203527	Hs.18747	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	
6432	>10	X89066	Hs.94413	ESTs	Transient receptor potential channel 1
37001	>10	AA443311	Hs.95959	ESTs	
4530	>10	U52101	Hs.9599	Human YMP mRNA complete cds	
19489	>10	H27852	Hs.29137	ESTs	
28483	>10	C14270	Hs.66357	ESTs	
19801	>10	H57357	Hs.18767	ESTs	Weakly similar to unknown protein [H.sapiens]
24672	>10	Z38300	Hs.124952	ESTs	
31153	>10	N63869	EST - RC_N63868	EST - RC_N63868	
40250	>10	H82451	Hs.110	Solute carrier family 3 (cystine dibasic and neutral amino acid transporters activator of cystine dibasic and neutral amino acid transport) member 1	
23028	>10	H17215	Hs.6952	ESTs	
28072	>10	AA480886	Hs.86583	ESTs	
11868	>10	AA262556	Hs.28302	ESTs	ESTs Weakly similar to centaurin alpha [H.norvegicus]
35359	>10	AA390951	Hs.112661	ESTs	ESTs Moderately similar to PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR [H.sapiens]
4285	>10	U35139	Hs.50130	Human NECNIN related protein mRNA complete cds	
4655	>10	U52969	Hs.80266	BRAIN SPECIFIC POLYPEPTIDE PEP-19	
26030	>10	AA235984	Hs.67469	ESTs	
2042	>10	L36051	Hs.1186	Thrombopoietin (myelopoietic leukemia virus oncogene ligand megakaryocyte growth and development factor)	
25262	>10	AA043501	Hs.10250	Homo sapiens short form transcription factor C-Maf (c-maf) mRNA complete cds	
34621	>10	AA291683	Hs.144599	ESTs	
42405	>10	W44682	Hs.106898	ESTs	

FIGURE 7 (CONT.)

41348	>10	R40395	Hs.112125	Leothin-cholesterol acyltransferase
14194	>10	A403945	Hs.25632	ESTs Weakly similar to PNG gene [H.sapiens]
4453	>10	U43916	Hs.79368	Human epithelial membrane protein (CL-20) mRNA complete cds
42758	>10	Z41411	Hs.107040	ESTs
2098	>10	L39009	EST - L39009	ESTs
33637	>10	AA029533	Hs.29283	ESTs
10649	>10	AA029687	Hs.94554	ESTs
1220	>10	HG37333-	Hs.124994	EST - HG37333-4T.4003
39934	>10	H52185	Hs.109631	Human tyrosyl-RNA synthetase mRNA complete cds
7735	>10	AA232121	Hs.108800	ESTs
40382	>10	H95857	Hs.99145	ESTs
37170	>10	AA447779	Hs.99145	EST
18361	>10	AA223902	Hs.96599	EST
19366	>10	H19204	Hs.133466	ESTs
39429	>10	AA189865	Hs.108694	Glycophorin A
38021	>10	AA481059	Hs.105152	ESTs
5184	>10	U82169	Hs.87234	Human frizzled homolog (FZD3) mRNA complete cds
27863	>10	AA489923	Hs.70202	ESTs Weakly similar to F2382.4 [C.elegans]
37476	>10	AA455051	Hs.99386	EST
859	>10	D87468	Hs.40888	Human mRNA for KIAA0278 gene partial cds
27185	>10	AA410895	Hs.62248	ESTs
41010	>10	N80688	Hs.21639	Human APEG-1 mRNA complete cds
38241	>10	AA489076	Hs.105101	ESTs
22701	>10	R89477	Hs.34299	ESTs
12152	>10	AA291271	Hs.10386	ESTs Weakly similar to unorthophyngogen III synthase UROHIS [H.sapiens]
38913	>10	AA069531	Hs.120590	ESTs
34034	>10	AA192871	Hs.83780	Tropinin (skeletal fast)
37644	>10	AA459857	Hs.95503	EST
4173	>10	U29725	Hs.3080	Human BMK1 alpha kinase mRNA complete cds
16178	>10	AA009839	Hs.1632	CDZL RECEPTOR PRECURSOR
20527	>10	N54181	Hs.124044	ESTs
41918	>10	T28873	Hs.102243	ESTs
1525	>10	J04621	Hs.1501	Syndecan 2 (heparan sulfate proteoglycan 1 cell surface-associated thyroglycan)
19160	>10	H10208	Hs.30972	EST
18660	>10	AA055833	Hs.85152	ESTs Weakly similar to Nisus [M.musculus]
36927	>10	AA437259	Hs.104944	EST
1595	>10	K03207	Hs.103872	Salivary proline-rich protein
15574	>10	W38778	Hs.25216	ESTs
8885	>10	C00125	Hs.24332	ESTs Weakly similar to similar to deoxythiose-phosphate aldolase [C.elegans]
33995	>10	AA102845	Hs.139088	Homo sapiens FIP2 alternatively translated mRNA complete cds

FIGURE 7 (CONT.)

7949	AA283820	Hs.34586	ESTs	
10607	AA034918	Hs.85079	ESTs	
11670	AA252191	Hs.25196	Homo sapiens PAC clone DJ130H16 from 22q12.1-qter	
7354	AA082348	Hs.7858	ESTs	
4277	U34879	Hs.85279	ESTRADIAL 17 BETA-DEHYDROGENASE 1	
23214	T40805	Hs.11137	Human protein tyrosine phosphatase PTPCAAX1 (p11PTCAAX1) mRNA complete cds	
22209	R54594	Hs.25209	ESTs	
36151	AA118011	Hs.96744	ESTs	
23372	T59537	EST - RC_T59537	EST - RC_T59537	
42136	T72491	Hs.73849	Apolipoprotein C-III	
289	D16480	Hs.75990	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoadyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein) alpha subunit	
15974	Z36531	Hs.2659	H-sapient mRNA for fibrinogen-like protein (f119 protein)	
41379	R42233	Hs.105487	Homo sapiens mRNA for KIAA0673 protein partial cds	
34764	AA287370	Hs.890	Lymphoblastin-beta	
24027	W01875	Hs.5734	Homo sapiens mRNA for KIAA0679 protein partial cds	
35197	AA421156	Hs.97514	ESTs	
37211	AA448334	EST - RC_AA448334	EST - RC_AA448334	
27684	AA449625	Hs.57929	ESTs	
31790	N52779	Hs.50891	ESTs	
24515	Z38289	Hs.12701	ESTs	
16652	F03111	Hs.22505	ESTs	
16935	AA037433	Hs.46987	ESTs	
37815	AA469562	Hs.57699	ESTs	
6364	X83857	Hs.495	Prostaglandin E receptor 3 (subtype EP3) (alternative products)	
9334	C01833	Hs.20759	ESTs Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]	
16469	AA025728	Hs.61307	ESTs	
27034	AA400102	Hs.49051	ESTs	
42746	Z40846	Hs.124953	ESTs	
33598	AA399269	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
34805	AA291522	Hs.97250	EST	
15963	H89355	Hs.6598	ESTs	
31128	N63444	Hs.124566	ESTs	
22616	R81549	Hs.124954	ESTs	
12246	AA346198	Hs.14829	Homo sapiens mRNA for GABA-BR1a (NGE1a) receptor	
8777	AA459685	Hs.7974	ESTs	
13496	AA453034	Hs.21041	ESTs Highly similar to FIBROPELIN C PRECURSOR [Stongylocentrotus purpuratus]	
25512	AA086721	Hs.95611	ESTs	
29073	F12567	EST - RC_F12567	EST - RC_F12567	
5541	X07203	CD20 RECEPTOR	CD20 RECEPTOR	
41680	R82942	Hs.89751	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]	
		Hs.107755	ESTs Weakly similar to GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE [E.coli]	

FIGURE 7 (CONT.)

32343	>10	R00955	Hs.125052	ESTs
38335	>10	AA460916	Hs.112157	ESTs
41729	>10	R32456	Hs.05054	Hemoglobin gamma-G
36707	>10	AA434246	Hs.98002	EST
26491	>10	C14764	Hs.12382	ESTs
41702	>10	R06870	Hs.12353	ESTs
32246	>10	R52163	Hs.144526	ESTs
17314	>10	AA006467	Hs.107305	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [Homo sapiens]
30325	>10	N39867	Hs.44904	EST
19823	>10	H59562	Hs.9520	ESTs Highly similar to FORMYL-TETRAHYDROFOLATE DEHYDROGENASE [Rattus norvegicus]
42153	>10	T77729	Hs.89890	Pyruvate carboxylase
19321	>10	H17511	Hs.24953	ESTs
27110	>10	AA040484	Hs.81112	GTP synthetase
28831	>10	D59722	Hs.32924	ESTs
6333	>10	X82494	Hs.2853	Fibulin 2
37679	>10	AA460661	Hs.95652	ESTs
40829	>10	N64344	Hs.79362	Human clone 23839 mRNA sequence
15132	>10	H09343	Hs.27281	ESTs
19353	>10	H18706	Hs.31604	ESTs
10935	>10	AA121534	Hs.6923	ESTs Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]
11621	>10	AA243574	Hs.14691	ESTs
35538	>10	AA521370	Hs.104423	ESTs
30014	>10	R22139	Hs.30343	ESTs
4464	>10	N26740	Hs.42771	ESTs
3950	>10	U44429	Hs.16911	Human D33 (ND33) mRNA partial cds
36377	>10	U03877	Hs.75224	Human extracellular protein (S1-S) mRNA complete cds
35377	>10	AA428056	Hs.89450	ESTs
20437	>10	N50550	Hs.24587	Homo sapiens mRNA for Ets1 complete cds
1976	>10	K02100	Hs.117050	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR
42078	>10	T64891	Hs.144323	ESTs
27257	>10	AA418001	Hs.45146	ESTs Weakly similar to mitogen-activated kinase kinase A2 mRNA complete cds [H. sapiens]
30852	>10	N49846	Hs.46974	EST
3831	>10	U03090	Hs.290	Homo sapiens Ca2+-dependent phospholipase A2 mRNA complete cds
19026	>10	H04768	Hs.30464	Glycoprotein Ib (platelet) beta polypeptide
4752	>10	U59632	Hs.3847	CYCLOLIPID-DEPENDENT KINASE INHIBITOR 1
3768	>10	U09579	Hs.74984	Lymphocyte cytosolic protein 1 (L-plastin)
1437	>10	J02923	Hs.76506	AFPX-Tpox-X-5
33905	>10	AFPX-		
4310	>10	U37055	Hs.76034	Macrophage stimulating 1 (hepatocyte growth factor-like)
26923	>10	AA342302	Hs.55036	ESTs

FIGURE 7 (CONT.)

5520	X02256	Hs.119218	Integrin alpha 5 (fibronectin receptor alpha polypeptide)
37571	AA457409	Hs.99468	EST
38800	AA69052	Hs.112636	EST
27552	AA463700	Hs.47042	Homo sapiens CD39L3 (CD39L3) mRNA complete cds
27621	AA448242	Hs.56589	ESTs
38784	AA60888	Hs.2051	Testis specific protein Y-faked
291	D16532	Hs.73729	Very low density lipoprotein receptor
18014	AA173168	Hs.57672	ESTs Weakly similar to weakly similar to myosin heavy chain [C.elegans]
16720	AA044732	Hs.77208	ESTs
25336	AA053405	Hs.101404	ESTs
2547	M28609	Hs.1009	ATPase H+ transporting lysosomal (vacuolar proton pump) beta polypeptide 56/58kD isoform 1
39583	Hs6010	Hs.108144	ESTs Weakly similar to IIII ALL SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
13777	AA463504	Hs.6052	ESTs
13419	AA450038	Hs.22269	ESTs
1403	J00123	Hs.53557	PROENKEPHALIN A PRECURSOR
42073	W35362	Hs.103012	ESTs
21520	R28267	Hs.24258	ESTs
9766	M63509	Hs.73974	Glutathione S-transferase M2 (muscle)
35650	AA404271	Hs.22631	Human glutamate receptor (GLUR5) mRNA complete cds
42091	W69568	Hs.103156	ESTs
33512	Z41239	Hs.106980	ESTs
42473	W63731	Hs.122531	ESTs
25165	AA033780	Hs.75736	Apolipoprotein D
3712	C21481	Hs.34630	ESTs Moderately similar to IIII ALL SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
6214	U07520	Hs.59661	Human MAP kinase mRNA complete cds
31775	X77307	Hs.2507	5-HYDROXYTRYPTAMINE 2B RECEPTOR
23575	T80633	Hs.14794	ESTs
31775	N79765	Hs.50947	ESTs
5205	U82979	Hs.67846	Human clone HM18 monocyte inhibitory receptor precursor mRNA complete cds
22769	R94521	Hs.124693	ESTs
20958	H12674	Hs.9396	ESTs
41990	H61046	Hs.70405	EST Moderately similar to IIII ALL SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
25416	AA147537	Hs.4811	ESTs
36248	T33511	Hs.4844	ESTs
37255	H77734	Hs.105229	Homo sapiens roundabout 1 (robot) mRNA complete cds
21911	AA459218	Hs.95428	ESTs
23184	R43990	Hs.25320	ESTs
18225	T34622	Hs.8108	ESTs Weakly similar to HYPOTHETICAL 35.8 kD PROTEIN IN PRP16-SRP40 INTERGENIC REGION [S.cerevisiae]
	AA011305	Hs.10029	Cathepsin C

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FIGURE 7 (CONT.)

27766	>10	AA453656	Hs.58417	ESTs	
16071	>10	AA001426	Hs.40863	ESTs	
17343	>10	AA100152	Hs.5521	ESTs	
10643	>10	AA040154	Hs.32478	ESTs	
29335	>10	H65239	Hs.35122	ESTs	
34966	>10	AA344866	Hs.1255	Complement component 8 gamma polypeptide	
26303	>10	AA255483	Hs.58042	EST	
1030	>10	HG2416-		EST - HG2416-H12512	
28370	>10	AA009569	Hs.38550	ESTs Moderately similar to alfa subunit [H.sapiens]	
29303	>10	H65881	Hs.38427	ESTs	
21076	>10	N99976	Hs.8016	ESTs	
27100	>10	AA040231	Hs.28462	EST - RC_AA404231	
11329	>10	AA015669	Hs.74602	AQUAPORIN-CHIP	
4402	>10	U41518	Hs.5558	ESTs	
11050	>10	AA142919	Hs.5558	EST - RC_R38947	
22844	>10	R89847	Hs.39038	ESTs	
31581	>10	N71371	Hs.139119	ESTs	
7263	>10	AA074407	Hs.104638	EST - RC_AA621750	
20423	>10	N49308	Hs.104638	EST - RC_AA621750	
39264	>10	AA425598	Hs.24597	Homo sapiens chromosome 21q22.1 anonymous mRNA sequence	
36415	>10	AA031948	Hs.57548	ESTs	
16675	>10	AA455669	Hs.103233	ESTs	
37605	>10	AA521080	Hs.46785	ESTs	
28264	>10	T05325	Hs.18545	ESTs	
23886	>10	AA058485	Hs.33413	ESTs	
11781	>10	AA114250	Hs.48924	Homo sapiens mRNA for KIAA0512 protein complete cds	
25023	>10	C00808	Hs.107862	ESTs	
5903	>10	X15357	EST - X15357	ESTs	
5932	>10	AA036046	Hs.8009	ESTs	
7590	>10	R95858	Hs.35437	ESTs	
22763	>10	N86540	Hs.17713	ESTs	
10786	>10	AA047698	Hs.49168	ESTs	
37356	>10	AA456973	Hs.29738	Apolipoprotein D	
35957	>10	AA112537	Hs.59149	EST	
42729	>10	T71591	Hs.64624	ESTs	
34365	>10	AA261002	Hs.40735	ESTs	
33690	>10	Z38007	Hs.62246	ESTs	
8904	>10	AF002256	Hs.59150	Homo sapiens killer cell receptor (KIR103) mRNA allele ASD1 complete cds	
2859	>10	M32273	Hs.12256	Alysiuridase B	

FIGURE 7 (CONT.)

40909	>10	NR0004	Hs.48608	ESTs	
22377	>10	RC0090	Hs.28391	ESTs	
21208	>10	R07551	Hs.20023	EST	
27304	>10	AA421793	Hs.59608	Homo sapiens mRNA for zinc finger protein FPM315 complete cds	
3307	>10	NR0509	Hs.48678	BASIC TRANSCRIPTION FACTOR 82 KD SUBUNIT	
23370	>10	AA057556	Hs.28478	ESTs	
41423	>10	RC41717	Hs.22617	ESTs	
2570	>10	W27100	Hs.28353	Tyrosinase (tyrosinase-related protein 1A)	
14857	>10	AA020850	Hs.100300	ESTs Highly similar to ADENYLOSUCCINATE SYNTHETASE MUSCLE ISOZYME [Mus musculus]	
7023	>10	Z76231	EST - Z76231	EST - Z76231	
31051	>10	NR0598	Hs.48607	EST	
39200	>10	AA021546	Hs.112956	EST	
24712	>10	Z39652	Hs.27457	ESTs	
23296	>10	T32497	Hs.9444	ESTs Moderately similar to IIII ALLU CLASS A WARNING ENTRY IIII [H. sapiens]	
12826	>10	AA424606	Hs.134646	ESTs	
2199	>10	LA9169	Hs.73078	Human GOS3 mRNA complete cds	
27226	>10	AA416767	Hs.43498	ESTs	
7135	>10	AA028976	Hs.8175	ESTs	
17102	>10	AA074955	Hs.94970	EST - RC_AA074955	
38942	>10	AA009846	Hs.38336	Human mRNA for KIAA0306 gene partial cds	
29288	>10	H64973	Hs.54434	Interferon regulatory factor 5	
34336	>10	AA0250943	Hs.47681	ESTs	
30816	>10	N53596	Hs.65083	ESTs	
16739	>10	AA045461	Hs.113025	ESTs	
42317	>10	T97599	EST - L77563	EST - L77563	
2228	>10	L77563	Hs.47927	ESTs	
30692	>10	N55171	Hs.97951	ESTs	
35954	>10	AA412526	Hs.98467	ESTs	
38403	>10	AA425383	Hs.99559	ESTs	
36949	>10	AA441812	Hs.79630	Immunoglobulin-associated alpha	
41028	>10	R70212	Hs.111996	ESTs	
39175	>10	AA021076	EST - RC_AA460147	EST - RC_AA460147	
37557	>10	AA460147	Hs.98397	ESTs Weakly similar to precursor of major fibrous sheath protein [M. musculus]	
36279	>10	AA424242	Hs.2960	S100 calcium-binding protein A5 (formerly S100D)	
6834	>10	Z18894	Hs.107197	ESTs	
40562	>10	N33512	Hs.22636	ESTs	
13770	>10	AA463272	Hs.70362	Human clone 23839 mRNA sequence	
5101	>10	U79249	Hs.31305	Human translocin-like enhancer protein (TLE3) mRNA complete cds	
3355	>10	M99438	Hs.29790	ESTs	
8476	>10	AA442119			

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FIGURE 7 (CONT.)

34231	A2234327	Hs.75772	Glucocorticoid receptor
42046	T59148	Hs.50966	Carbamoyl-phosphate synthetase 1 mitochondrial
23913	T96123	Hs.17749	ESTs
37333	A4452158	Hs.75122	TRANSFORMING PROTEIN RHOB
27946	A4463434	Hs.42658	ESTs
34407	A2255523	EST - RC_A2255523	ESTs
16542	A0294228	Hs.61555	ESTs
6246	X78712	Hs.98008	Glycerol kinase 2 (testis specific)
8227	A339666	Hs.75709	Mannose-6-phosphate receptor (cation dependent)
3507	S78774	EST - S78774	ESTs
40907	N98330	Hs.25717	ESTs
33340	W79698	Hs.58550	ESTs
19079	H05371	Hs.20945	ESTs
3992	U19713	Hs.76384	Allograft inflammatory factor 1
36059	A4417083	Hs.99189	ESTs
37634	A4459892	Hs.99489	EST
41581	R62313	Hs.126270	ESTs Weakly similar to RTP90 [R:nervous]
38734	A4608792	Hs.112951	EST
37836	A4470135	Hs.112238	ESTs
21303	N22056	Hs.12610	ESTs
20125	A4400795	Hs.97459	ESTs
35516	A4284067	Hs.89267	EST
26771	N92735	Hs.59332	EST
33558	M27399	Hs.44	Phalloidin (heparin binding growth factor 6 neurite growth-promoting factor 1)
2830	N94926	Hs.110128	ESTs
42625	A3250845	Hs.87762	ESTs
26162	N94581	Hs.55052	ESTs
31988	A148213	Hs.71873	ESTs Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]
17763	R44949	Hs.22926	ESTs
18569	N79874	Hs.79915	ESTs
10020	N51105	Hs.112223	ESTs
30688	A4131918	Hs.69009	ESTs
17628	A4423970	Hs.98378	ESTs
39280	D18227	Hs.3918	Hepocidin-like 1
28123	A3433698	Hs.20987	ESTs
34535	A3379391	Hs.104405	EST
28100	H01428	Hs.82380	ESTs
24122	W46947	Hs.4186	ESTs
19894	H05942	Hs.35030	ESTs

FIGURE 7 (CONT.)

22587	>10	T10258	Hs.25420	ESTs	
5985	>10	X64728	Hs.34514	H.sapiens CHML mRNA	
42461	>10	W60008	Hs.89717	Human preprocarboxypeptidase A2 (proCPA2) mRNA complete cds	
5422	>10	X00588	Hs.71432	Epidermal growth factor receptor	
16603	>10	AA034386	Hs.144627	ESTs	
33369	>10	W61607	Hs.59853	EST	
6931	>10	Z46788	Hs.3232	H.sapiens mRNA for cyclin II	
19324	>10	H17618	Hs.28180	ESTs	
32150	>10	R41835	Hs.3957	ESTs	
39667	>10	H58415	Hs.102160	EST	
17658	>10	AA165817	Hs.72639	ESTs	
18324	>10	AA59437	Hs.29385	ESTs HIGHLY similar to MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 [Saccharomyces cerevisiae]	
38559	>10	H-G2280-	EST - H32260-HT2349		
1006	>10	T79638	Hs.105618	ESTs	
23552	>10	AA486897	Hs.137530	ESTs	
38228	>10	HG2705-	EST - H32705-HT2801		
1066	>10	T91283	EST - RC_T91283		
23815	>10	U57099	Human APEG-1 mRNA complete cds		
4689	>10	N67796	Hs.144212	ESTs	
31300	>10	AA399633	Hs.24872	ESTs	
12389	>10	AA279682	Hs.142452	ESTs Moderately similar to snRNP protein B [H.sapiens]	
34539	>10	N38584	Hs.17404	ESTs	
20359	>10	AA235868	Hs.87594	ESTs	
28070	>10	AA488659	Hs.105696	ESTs	
38210	>10	AA235874	Hs.89888	PUTATIVE DNA BINDING PROTEIN A20	
26025	>10	U171207	Hs.29279	Human sapiens clone 24534: eyes absent homolog (Eab1) mRNA partial cds.	
4978	>10	U81152	Hs.84171	THROMBOPOIETIN RECEPTOR PRECURSOR	
4935	>10	S78467	EST - S78467		
3501	>10	AA505136	Hs.12420	ESTs	
14281	>10	N50588	Hs.54843	EST	
31859	>10	RC1388	EST - RC_R01388		
41104	>10	U69595	Human DNA binding protein FKHL15 (FKHL15) mRNA complete cds		
5293	>10	S41957	EST - S41957		
3543	>10	AA443558	Hs.90060	ESTs	
27515	>10	AA036753	Hs.79484	Human sapiens mRNA for KIAA0525 protein partial cds	
7152	>10	AA010328	Hs.39379	ESTs	
16197	>10	N24772	Human sapiens putative transmembrane protein (CLN5) mRNA complete cds		
20716	>10	W62015	Hs.73166	Treacher Collins syndrome susceptibility protein	
33586	>10	AA418392	Hs.46784	ESTs	
27265	>10	AA402000	ESTs Weakly similar to GS3785 [H.sapiens]		
12453	>10				

FIGURE 7 (CONT.)

35302	>10	AA424652	Hs.124965	ESTs	
23192	>10	T40448	Hs.8204	ESTs	
17423	>10	AA114071	Hs.26270	ESTs	
23464	>10	T67026	Hs.13019	ESTs	
42752	>10	Z41697	Hs.106296	ESTs	
35268	>10	T56470	Hs.115190	Chromogranin A (parathyroid secretory protein 1)	
12905	>10	AA424331	Hs.29640	ESTs	
25379	>10	AA058863	Hs.111841	Human adenovyl cyclase-associated protein homolog CAP2 (CAP2) mRNA complete cds	
39318	>10	C20617	Hs.108845	Homo sapiens mRNA for KIAA0515 protein partial cds	
28699	>10	H97938	Hs.75772	Glucocorticoid receptor	
17697	>10	AA160530	Hs.72447	ESTs	
35819	>10	AA411011	Hs.8038	ESTs	
36638	>10	AA436163	Hs.95851	Homo sapiens Pg12 (PG12) mRNA complete cds	
28511	>10	H94043	Hs.41949	ESTs	
19590	>10	H46167	Hs.31542	ESTs	
33221	>10	W70305	Hs.64856	ESTs	
18940	>10	F10265	Hs.13287	ESTs	
2350	>10	M27533	EST - M27533		
7274	>10	A032171	Hs.8261	ESTs	
18524	>10	H25569	Hs.83466	Homo sapiens clone 23576 mRNA sequence	
43971	>10	N33559	Hs.103102	ESTs Weakly similar to WWP2 [H.sapiens]	
31176	>10	N84191	Hs.46594	ESTs	
23894	>10	N20379	Hs.43296	ESTs	
22201	>10	R54416	Hs.140932	ESTs	
29718	>10	A0328393	Hs.89617	ESTs	
32463	>10	T16497	Hs.65339	EST	
37179	>10	AA448904	Hs.99150	ESTs	
17860	>10	A1169723	Hs.72754	ESTs	
21654	>10	R44449	Hs.46778	ESTs	
39782	>10	AA435846	EST - RC_AA435846		
34035	>10	AA104651	Hs.110575	ESTs	
39102	>10	AA020974	Hs.110882	EST	
25263	>10	AA035217	Hs.41271	ESTs	
23869	>10	T18528	Hs.16399	ESTs	
32435	>10	T15623	Hs.62626	ESTs	
15440	>10	W27301	Hs.111652	ESTs Moderately similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA [Thermonaspora curvata]	
19004	>10	H33289	Hs.30390	EST	
27839	>10	AA405309	Hs.59831	ESTs	
18848	>10	F10338	Hs.103009	ESTs Moderately similar to FOG [M.musculus]	
13112	>10	AA435866	Hs.10397	ESTs	

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FIGURE 7 (CONT.)

1850	>10	L17325	Hs.276	Human pre-TNK cell associated protein (1D12A2) mRNA complete cds
9101	>10	C17938	Hs.25536	ESTs
2807	>10	M52710	Hs.87428	Laminin gamma 1 (formerly LAMB2)
3383	>10	S57153	Hs.91797	Retinoblastoma-binding protein 1 (alternative products)
23142	>10	T25444	Hs.101248	ESTs
5367	>10	U65019	Hs.30941	Myasthenic syndrome antigen B (human fetal brain mRNA 3477 nt)
32205	>10	R44234	Hs.75169	ESTs
28515	>10	A2262972	Hs.87298	ESTs
15332	>10	W24127	Hs.16003	ESTs Weakly similar to keratin 8 type II cytoskeletal embryonic (M.musculus)
34183	>10	A2322251	Hs.126630	ESTs
6392	>10	X65753	Hs.25283	CELL DIVISION PROTEIN KINASE 8
33784	>10	Z40889	Hs.65973	ESTs
33474	>10	W87484	Hs.50429	ESTs
34864	>10	A3344854	Hs.96837	ESTs
14554	>10	A621414	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
22640	>10	R83964	Hs.33416	EST - U38372
4339	>10	U38372		EST - U38372
37557	>10	A4456668	Hs.41548	Human MHC Class I region proline rich protein mRNA complete cds
4937	>10	U68385	Hs.117313	Human MHC Class I region proline rich protein mRNA complete cds
30785	>10	N53043	Hs.47606	ESTs
30688	>10	N59432	Hs.48382	EST
33581	>10	A4181935	Hs.104059	EST
2265	>10	M11591		EST - M11591
24315	>10	W64413	Hs.23017	ESTs
38752	>10	A608852	Hs.112603	EST
5119	>10	U79271	Hs.7571	Human clones 23920 and 23921 mRNA sequence
15037	>10	U44798	Hs.93502	Human U1 snRNP binding protein homolog mRNA complete cds
37045	>10	A4460000	Hs.99043	ESTs
37527	>10	A4459382	Hs.105042	ESTs
21835	>10	R44477	Hs.22546	ESTs
18669	>10	F03889	Hs.27278	ESTs Highly similar to PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A [Bos taurus Sus scrofa]
22737	>10	R92512		EST - RC_R92512_s
30727	>10	N51987	Hs.47390	EST
16096	>10	A4001879	Hs.59590	EST
23293	>10	T52201	Hs.9410	ESTs
5294	>10	U90085	Hs.79351	Human two P-domain K ⁺ channel TWIK-1 mRNA complete cds
17768	>10	A4148923	Hs.93675	ESTs
25549	>10	A4101056		EST - RC_AA101056
84	>10	AF001359		EST - AF001359.f
4856	>10	U85083		Human msng1-related gene 1 (mg1) mRNA complete cds

FIGURE 7 (CONT.)

7597	>10	AA214730	Hs.107256	ESTs	
36596	>10	AA246335	Hs.98416	ESTs	
17490	>10	AA125781	Hs.57489	ESTs	
36576	>10	AA442779	Hs.98983	ESTs	
10425	>10	AA010610	Hs.16446	ESTs	
41198	>10	R11664	Hs.20526	ESTs	
42285	>10	T94409	EST - RC_T94409	EST	
33185	>10	V69435	Hs.58009	EST	
13974	>10	AA473269	Hs.21107	ESTs	
19869	>10	H61560	EST - RC_H61560	EST	
1378	>10	H6391	EST - HG31-H1831	EST	
621	>10	D63413	Hs.26988	Human mRNA for rod photoreceptor protein complete cds	
5348	>10	U52169	Hs.82304	Human mRNA for rod photoreceptor protein complete cds	
6029	>10	X68333	Hs.77600	QUANTAL CYCLASE SOLUBLE BETA-1 CHAIN	
22108	>10	R59272	Hs.26236	ESTs	
24609	>10	Z384003	Hs.26615	ESTs	
37198	>10	AA448226	EST - RC_AA448226	EST	
26151	>10	AA259356	Hs.109509	ESTs	
3939	>10	X62335	Hs.14244	Decylglycerol kinase alpha (50kD)	
32933	>10	AA019803	Hs.06992	ESTs	
32656	>10	AA069660	Hs.41585	ESTs	
20070	>10	H98854	Hs.20423	ESTs	
17117	>10	AA139541	Hs.17647	EST	
20059	>10	H96768	Hs.13121	ESTs	
40935	>10	N74604	Hs.12454	ESTs	
10194	>10	R53945	Hs.11533	ESTs Weekly similar to putative type III alcohol dehydrogenase [D.melanogaster]	
40200	>10	R67229	Hs.82363	Gonadotrophin-releasing hormone (releasing hormone)	
34983	>10	AA347417	Hs.98989	EST	
23543	>10	T75203	Hs.14480	ESTs	
12770	>10	AA421778	Hs.0851	ESTs	
25885	>10	AA017518	Hs.115241	Homo sapiens G protein beta 5 subunit mRNA complete cds	
37746	>10	AA463627	Hs.96598	ESTs	
2370	>10	M16505	Hs.73676	STERYL-SULFATASE PRECURSOR	
31244	>10	N60662	Hs.49112	EST	
31716	>10	N75307	Hs.30628	ESTs Weekly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP7 [Rattus norvegicus]	
28308	>10	AA599959	Hs.59163	ESTs	
2220	>10	L76987	Hs.83070	Homo sapiens Gb14 mRNA complete cds	
12404	>10	AA400282	Hs.23786	ESTs	
41050	>10	N92882	Hs.109494	ESTs Weekly similar to putative progesterone binding protein [H.sapiens]	
2407	>10	M18737	Hs.90708	GRANZYME A PRECURSOR	

FIGURE 7 (CONT.)

23462	>10	T66948	Hs.12592	ESTs
18514	>10	F02418	Hs.107614	ESTs
40553	>10	N32060	Hs.104010	Homo sapiens CAC-1a 7 mRNA complete cds
27826	>10	AA455949	Hs.61232	ESTs
207	>10	D12763	Hs.66	Suppression of tumorigenicity 2
41064	>10	N93508	Hs.102923	EST
10845	>10	AA084405	Hs.106313	ESTs
21813	>10	RA22039	Hs.23284	Weakly similar to P24 protein [M.musculus]
19463	>10	AA233151	Hs.81796	ESTs
17507	>10	AA128419	Hs.74876	ESTs
23957	>10	T97487	Hs.18070	ESTs
13317	>10	AA448242	Hs.30095	ESTs
29550	>10	H90133	Hs.41352	ESTs
33068	>10	AA620411	Hs.141503	Small inducible cytokine A5 (RANTES)
28520	>10	AA280413	Hs.85643	Spleen focus forming virus (SFFV) proviral integration oncogene sp1
37675	>10	AA460377	Hs.99516	ESTs
31437	>10	N68921	Hs.45673	ESTs
32657	>10	T66967	Hs.76889	ESTs
34952	>10	AA342828	Hs.73734	PLATELET GLYCOPROTEIN V PRECURSOR
28475	>10	AA262264	Hs.87640	ESTs
41827	>10	T15445	Hs.99491	Hs.sapiens mRNA for F2583.3 kinase like protein from C.elegans
20073	>10	H98985	Hs.111911	ESTs
42336	>10	T99713	Hs.135933	ESTs
28412	>10	AA258224	Hs.86646	ESTs
21352	>10	R15890	Hs.21745	ESTs
22583	>10	R79239	Hs.29855	EST
34020	>10	AA191543	Hs.144302	EST
25913	>10	AA181106	EST - RC_AA181106	
82	>10	AF000569	Hs.110903	Homo sapiens transmembrane protein mRNA complete cds
37531	>10	AA456140	Hs.95235	ESTs
13314	>10	AA448169	Hs.6728	ESTs
31430	>10	N68610	EST - RC_N68610	
35570	>10	N49587	Hs.46633	EST
7302	>10	AA089688	Hs.103668	EST
27732	>10	AA452187	Hs.55778	ESTs
22553	>10	R73458	Hs.140996	ESTs
31079	>10	N62959	Hs.48682	EST
35470	>10	AA400363	Hs.97803	EST Weakly similar to precursor polypeptide [H.sapiens]
37102	>10	AA445889	Hs.119316	ESTs
203	>10	D12620	Hs.106242	CYTOCHROME P450 IVF3

FIGURE 7 (CONT.)

11427	10	AA233277	Hs.74547	ESTs	EST - RC_AA079084
24159	10	W57862	Hs.21289	ESTs	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds
17870	10	AA157772	Hs.72185	ESTs	EST - RC_AA063386
5302	10	U60543	Hs.75941	Human butyrophilin (BTF-1) mRNA complete cds	EST - RC_AA063386
27256	10	AA417988	Hs.62781	ESTs	EST - RC_AA063386
2219	10	L76570	Hs.109510	Homo sapiens rai17 mRNA complete cds	EST - RC_AA063386
30858	10	N55081	Hs.47915	EST	EST - RC_AA063386
8870	10	AB002367	Hs.13355	Human mRNA for KIAA0369 gene complete cds	EST - RC_AA063386
40870	10	N67262	Hs.358	Zinc finger protein 135 (clone pZ-17)	EST - RC_AA063386
11811	10	AA228130	Hs.11530	ESTs	EST - RC_AA063386
33254	10	W72633	Hs.58187	ESTs	EST - RC_AA063386
17162	10	AA079084	Hs.56589	Homo sapiens glycogenin-2 gamma (glycogenin-2) mRNA complete cds	EST - RC_AA063386
24392	10	W85588	Hs.57760	ESTs	EST - RC_AA063386
27456	10	AA430539	Hs.57760	ESTs	EST - RC_AA063386
25419	10	AA069366	Hs.60548	ESTs	EST - RC_AA063386
7100	10	AA012885	Hs.50050	ESTs	EST - RC_AA063386
31586	10	N71571	Hs.43902	EST	EST - RC_AA063386
25995	10	N26101	Hs.55015	EST	EST - RC_AA063386
31973	10	N93875	Hs.82813	Colony-stimulating factor 1 (M-CSF)	EST - RC_AA063386
36159	10	AA419279	Hs.7159	ESTs	EST - RC_AA063386
12419	10	AA400868	Hs.62592	ESTs	EST - RC_AA063386
27076	10	AA401630	Hs.75952	ESTs	EST - RC_AA063386
26251	10	AA504512	Hs.64310	Human Interleukin-11 receptor alpha chain mRNA complete cds	EST - RC_AA063386
4219	10	U32324	Hs.87306	ESTs	EST - RC_AA063386
27891	10	AA465650	Hs.99539	ESTs	EST - RC_AA063386
37702	10	AA481119	Hs.54421	Bisphosphonate receptor B2	EST - RC_AA063386
25251	10	AA400792	Hs.87677	ESTs	EST - RC_AA063386
27064	10	AA401253	Hs.95698	ESTs	EST - RC_AA063386
37562	10	AA458688	Hs.12354	ESTs	EST - RC_AA063386
35819	9	F10640	Hs.48614	EST	EST - RC_AA063386
31053	9	N62724	Hs.58955	ESTs	EST - RC_AA063386
33338	9	W79524	Hs.10476	EST	EST - RC_AA063386
23358	9	T59005	Hs.10879	ESTs	EST - RC_AA063386
8240	9	AA397841	Hs.26159	EST	EST - RC_AA063386
21778	9	FA1389	Hs.48933	ESTs	EST - RC_AA063386
31168	9	N53965	Hs.89890	Prostate carboxylase	EST - RC_AA063386
34440	9	S72370	Hs.93692	EST	EST - RC_AA063386
25930	9	AA164628	Hs.10735	ESTs	EST - RC_AA063386
29871	9	N26657	Hs.10735	ESTs	EST - RC_AA063386
39771	9	H17453	Hs.10735	ESTs	EST - RC_AA063386

FIGURE 7 (CONT.)

21481	R26141	Hs.24032	ESTs highly similar to transmembrane receptor [H. musculus]
10887	Hs.22971	ESTs	
31431	AA101632	ESTs	
9	N68666	Hs.76758	ESTs
30756	N52398	Hs.39252	ESTs
35829	AA114138	Hs.74835	Dihydrodipicolinate dehydrogenase (E3 component of pyruvate dehydrogenase complex 2-oxo-glutarate complex branched chain keto acid dehydrogenase)
24540	Z38435	Hs.19235	ESTs
37500	AA455474	Hs.100530	ESTs
15007	H03358	EST - RC_H03358	
42950	V92272	Hs.25601	Homo sapiens zinc-finger helixase (hZFH) mRNA complete cds
16705	AA043675	Hs.62633	EST
24372	H94647	Hs.102329	ESTs
40275	V87423	Hs.35598	ESTs
9011	C01394	Hs.106823	Homo sapiens clone 24818 mRNA sequence
40780	N95668	Hs.108107	ESTs
11717	AA079331	EST - RC_AA079331	
22878	N70305	Hs.34492	ESTs
38140	AA488273	Hs.100472	ESTs
3480	S77763	Hs.75543	Homo sapiens NF-E2 protein (NF-E2) mRNA complete cds
39112	AA820724	Hs.112890	ESTs
27347	AA424940	Hs.43590	ESTs
14747	D60854	Hs.34882	ESTs
23559	T82307	EST - RC_T82307	
23979	T98262	EST - RC_T98262	
27759	AA453472	Hs.95111	ESTs
35691	AA432381	Hs.97357	ESTs Moderately similar to NITRIC OXIDE SYNTHASE INDUCIBLE (H-sapiens)
25782	A4264181	Hs.85310	ESTs
26818	A4265145	Hs.50448	ESTs
22334	R61290	Hs.25670	ESTs
23852	N22895	Hs.42929	ESTs
22945	T10134	Hs.9877	ESTs
30518	N50556	Hs.93596	Homo sapiens mRNA for KIAA0858 protein complete cds
29715	H98700	Hs.63887	ESTs Highly similar to mesate protein LR11 (H-sapiens)
37655	AA457023	EST - RC_AA457023	
22364	T52652	Hs.9392	EST
31001	N82200	Hs.47568	ESTs
17841	AA188109	Hs.69180	ESTs
3476	S76892	Hs.104005	Var.2 oncogene
11595	AA303139	Hs.4883	ESTs
15002	H04822	Hs.30494	EST
25933	R24182	Hs.53877	ESTs

FIGURE 7 (CONT.)

26222	9	AA260431	Hs.38756	ESTs	
4289	9	U35795	Hs.37138	Human repressor transcriptional factor (ZNF95) mRNA complete cds	
42034	9	T56281	Hs.110440	Human metallothionein (MT)-F gene	
30447	9	N47439	Hs.44603	ESTs	
25238	9	AA039588	Hs.46003	EST - RC_AA039588	
20238	9	N30077	Hs.14855	ESTs	
30232	9	N34503	Hs.44600	ESTs	
17017	9	AA069920	EST - RC_AA069920		
11845	9	AA259064	ESTs Weakly similar to unknown [S. cerevisiae]		
30229	9	N34457	Hs.10839	EST - RC_N34457	
30737	9	N82137	Hs.47442	EST	
30655	9	N49259	EST - RC_N49259		
981	9	HG2139	EST - HG2139-IT2208_1		
30498	9	N48925	Hs.33956	EST	
40434	9	N21461	EST - RC_N21461		
38768	9	AA435624	Hs.35594	Homo sapiens BAC clone RG113D17 from 7p14-p15	
28991	9	F04852	Hs.66195	ESTs	
25942	9	AA034167	Hs.87267	ESTs	
30466	9	N47251	Hs.57485	ESTs	
13017	9	H17476	Hs.16161	ESTs Weakly similar to dual specificity phosphatase [H. sapiens]	
13655	9	AA270086	Hs.43309	ESTs Highly similar to S-ACTYL FATTY ACID SYNTHASE THIOESTERASE MEDIUM CHAIN [Rattus norvegicus]	
23446	9	T65932	Hs.11722	EST	
24446	9	V93273	Hs.32070	ESTs Weakly similar to isopentenyl-diphosphate Delta-isomerase [H. sapiens]	
7353	9	AA107624	Hs.63570	ESTs Highly similar to PROTEIN COCH2HS [Homo sapiens]	
22776	9	R101722	Hs.35372	ESTs Weakly similar to IIR ALU CLASS B WARNING ENTRY III [H. sapiens]	
16439	9	AA024495	Hs.47964	Homo sapiens Shab-related delayed-rectifier K ⁺ channel alpha subunit (KCNK3) mRNA complete cds	
42355	9	N42733	Hs.08570	ESTs	
23860	9	Hs.16357	ESTs		
7441	9	T37969	EST - RC_T37969		
7111	9	AA018804	Hs.125175	ESTs Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]	
6200	9	X86163	Hs.54421	Bradykinin receptor B2	
42474	9	V93747	Hs.09510	H-sapiens TTF mRNA for small G protein	
11425	9	AA232357	Hs.23511	Homo sapiens mRNA for Hc-5 partial cds	
27039	9	AA402277	Hs.46949	ESTs	
32206	9	R44586	Hs.91703	ESTs	
13310	9	W19098	Hs.7921	ESTs	
36901	9	AA431337	Hs.95017	ESTs	
463	9	D88462	EST - D88462		
31674	9	N74357	Hs.50462	ESTs	
31182	9	N64339	Hs.48595	EST	

FIGURE 7 (CONT.)

13469	8	AA453458	Hs.7301	ESTs	
37514	8	AA455914	Hs.1019	Parathyroid hormone receptor 1	
5996	8	X85644	Hs.7593	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2	
962	8	HG180-	EST - HG180-HT180		
40760	8	N62328	Hs.3786	Glutamate receptor metabotropic 3	
25700	8	AA131512	Hs.103820	EST	
36880	8	AA438705	Hs.98895	ESTs	
2809	8	M55267	Hs.41948	EV2A PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE 2A PROTEIN	
5620	8	X14885	Hs.2025	Transforming growth factor beta 3	
32051	8	AA038325	Hs.47200	ESTs	
16643	8	R01450	Hs.91061	ESTs	
33550	8	W90617	Hs.50120	ESTs	
6177	8	X75635	Hs.118894	33 MD HOUSEKEEPING PROTEIN	
33000	8	W45531	Hs.94542	ESTs	
20066	8	H98701	Hs.4935	ESTs	
4590	8	U50534	Hs.30649	Human infant brain mRNA clone 13dNA73	
37199	8	AA448257	Hs.07127	ESTs	
24601	8	Z38944	Hs.25903	ESTs	
33589	8	W93074	Hs.59342	ESTs	
37389	8	AA453468	Hs.99330	ESTs	
5801	8	X55448	Hs.3118	H.sapiens mRNA for 2.19 gene	
28748	8	D25912	Hs.74832	ESTs	
40070	8	H72592	Hs.77554	ESTs	
40367	8	H98957	Hs.75520	Human mRNA for KIA0041 gene partial cds	
33609	8	W93585	Hs.59476	ESTs	
24502	8	Z38214	Hs.26946	ESTs	
11129	8	AA158673	Hs.15970	ESTs	
7144	8	AA038569	Hs.95154	ESTs	
26594	8	C21221	Hs.08519	ESTs Highly similar to METALLOTHIONEIN [Equus caballus]	
22165	8	R52822	Hs.22003	ESTs	
31987	8	N94551	Hs.55000	ESTs	
32470	8	T15956	Hs.65298	EST	
39842	8	AA509152	Hs.91379	PTB-ASSOCIATED SPLICING FACTOR	
40438	8	N21694	Hs.60500	Human mRNA for KIA0081 gene partial cds	
34471	8	AA258943	Hs.111376	ESTs	
41571	8	R61005	Hs.115170	Homo sapiens mRNA for Gail14 protein	
31417	8	N69435	Hs.49516	ESTs	
23951	8	T97318	Hs.18037	ESTs	
7832	8	AA240280	Hs.25445	ESTs	
27628	8	AA461063	Hs.25769	ESTs Moderately similar to zinc finger protein [P. corvegius]	

FIGURE 7 (CONT.)

10108	7	R25069	Hs.23760	ESTs	
29178	7	AA251153	Hs.27910	Homo sapiens centrosomal Ndk2-associated protein 1 (C-NAP1) mRNA complete cds	
36428	7	AA427805	Hs.96551	Human cardiac myosin binding protein-C (MyBP-C) gene complete cds	
29608	7	N21032	Hs.42931	EST	
24837	7	Z41186	Hs.27997	ESTs	
24909	7	Z98492	Hs.27250	ESTs	
26333	7	AA258075	Hs.82980	Homo sapiens regulator of G protein signaling 10 mRNA complete cds	
11507	7	AA235465	Hs.29161	ESTs	
40387	7	H95460	Hs.108873	ESTs	
16112	7	AA004377	Hs.91113	Human bcl-2 (BCL2) mRNA complete cds	
25413	7	AA065096		EST - RC_A065096	
13322	7	AA443844	Hs.20687	ESTs	
27236	7	AA417037	Hs.67905	ESTs	
21694	7	R36844	Hs.129872	ESTs	
9924	7	D57112	Hs.15301	ESTs Weakly similar to weakly similar to ANK repeat region of Fowlpox virus SamH1-ort protein [C.elegans]	
16886	7	AA057119	Hs.5091	Homo sapiens IxosB (D01) mRNA partial cds	
20083	7	H98879	Hs.28029	ESTs Highly similar to EPIDERMAL GROWTH FACTOR PRECURSOR [Mus musculus]	
39651	7	N51029	Hs.39872	ESTs	
27382	7	R62447	Hs.22133	ESTs	
	7	R32345	Hs.22076	ESTs	
21658	7	R37559	Hs.23390	ESTs	
21223	7	R03175	Hs.110130	Homo sapiens chromosome 19 centromere F22229	
13405	7	AA46554	Hs.1339	Collagen type IV alpha 2	
30227	7	AA50016	Hs.25722	ESTs Weakly similar to KRUPPEL-RELATED ZINC FINGER PROTEIN 1 [Homo sapiens]	
30117	7	N50740	Hs.47111	ESTs	
31344	7	R30824	Hs.44227	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	
38119	7	N67236		EST - RC_N67236	
33297	7	AA469714	Hs.105669	ESTs	
30952	7	R73161	Hs.107115	ESTs	
9823	7	Z30356	Hs.82491	CD89 antigen (early T cell activation antigen)	
27842	7	N44893	Hs.24550	ESTs	
34845	7	AA483237	Hs.13021	ESTs	
28629	7	AA253420	Hs.35464	ESTs Moderately similar to transcription enhancer factor TEF1 [H.sapiens]	
15059	7	N21460	Hs.43005	ESTs	
40441	7	U30331	Hs.65260	Human interferon regulatory factor 7 (humirf7) mRNA complete cds	
25095	7	N22053	Hs.112063	ESTs	
2841	7	AA016837	Hs.105558	ESTs	
1945	7	M62640	Hs.82542	Acylphosphatase (neutrophil)	
42648	7	L25978	Hs.89649	Epoxide hydrolase 1 microsomal (xenobiotic)	
	7	W62150	Hs.79310	Human GAP SH3 binding protein mRNA complete cds	

FIGURE 7 (CONT.)

7	H40696	Hs.33750	ESTs
7	N20939	Hs.38756	ESTs
7	W26592	Hs.39330	ESTs
7	H38627	Hs.107696	ESTs
7	T97910	Hs.18184	EST
7	H97012	Hs.11090	ESTs Weakly similar to L8004.7 gene product [S.cerevisiae]
7	AA214510	Hs.89518	ESTs
7	R67370	Hs.28758	ESTs
7	N48294	Hs.46890	EST
7	AA287057	Hs.48820	ESTs
7	V666075	Hs.38715	ESTs
7	N67990	Hs.49421	ESTs
7	Z64721	Hs.75792	Hemoglobin alpha 1
6	V86996	Hs.59134	EST
6	U64320	Hs.123021	Human Y5 receptor mRNA complete cds
6	R38518	Hs.124295	EST
6	AA406320	Hs.21702	ESTs
6	T92951	Hs.110422	ESTs
6	R38475	Hs.21408	ESTs
6	AA121704	Hs.69494	ESTs
6	AA126673	Hs.110341	ESTs
6	T67324	Hs.91021	EST
6	S73840	Hs.931	H-spleins mRNA for fast 2a myosin heavy chain (3' end)
6	H52090-	EST - HG2090-HT2152	EST - HG2090-HT2152
6	AA346866	EST - AA346866	EST - AA346866
6	AA389522	Hs.97671	ESTs Weakly similar to T04A4.9 [C.elegans]
6	T91047	Hs.126785	ESTs
6	HG1486-	Hs.97349	EST - HG1486-HT1496
6	AA412106	Hs.94000	ESTs
6	AA019034	Hs.72157	ESTs
6	AA438613	Hs.29323	ESTs
6	R73036	Hs.96200	ESTs Weakly similar to T04A4.9 [C.elegans]
6	AA149889	Hs.96200	ESTs Weakly similar to A-kinase anchor protein 95 AKAP95 [R.norvegicus]
6	AA437346	Hs.2987	SHB adaptor protein (e Src homology 2 protein)
6	AA406058	Hs.97999	EST
6	AA430002	Hs.12044	ESTs
6	AA152323	Hs.71947	ESTs
6	AA015799	Hs.33792	ESTs
6	V956102	Hs.71218	ESTs
6	N50827	Hs.25275	ESTs

FIGURE 7 (CONT.)

23357	6	A4605120	Hs.50185	ESTs Weakly similar to The KIAA0147 gene product is related to adenylyl cyclase. [H.sapiens]
23322	6	A4007391	Hs.110227	ESTs
23334	6	H68159	Hs.28310	ESTs
23148	6	A4498975	Hs.6433	Homo sapiens clone 24523 mRNA sequence
30744	6	N52185	Hs.105385	H.sapiens mRNA for arginine methyltransferase
27577	6	A442090	Hs.119295	ESTs
33472	6	W87489	Hs.58952	ESTs
25887	6	AA1130957	Hs.100119	ESTs
10549	6	AA027317	Hs.19136	ESTs Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]
32836	6	W23631	Hs.55426	ESTs
17025	6	AA070160	EST - RC_AA070160	
22939	6	T110070	Hs.4217	Homo sapiens mRNA for KIAA0667 protein partial cds
15903	6	X52332	Hs.104115	Human Kozf gene for zinc finger protein
34618	6	AA282143	Hs.59094	H.sapiens mRNA for melanoma growth regulatory protein MIA
11074	6	AA148893	Hs.29068	ESTs
12212	6	AA297746	Hs.22654	ESTs
16102	6	AA002150	Hs.58972	ESTs
31340	6	N67197	Hs.50125	EST
19459	6	H24317	Hs.6526	ESTs
17533	6	AA127098	Hs.71057	EST
22017	6	R46597	Hs.22703	ESTs
23387	6	T87519	Hs.16075	ESTs Weakly similar to no similarities to reported gene products [H.sapiens]
30298	6	N35130	Hs.44792	EST Weakly similar to hypothetical protein [H.sapiens]
28973	6	F04014	Hs.65996	ESTs
17042	6	AA070397	EST - RC_AA070397	
20817	6	N89523	Hs.37630	ESTs
18430	6	AA332138	Hs.118898	ESTs
28493	6	C14820	Hs.67186	EST
30497	6	N48302	Hs.46952	EST
32502	6	T16896	Hs.65373	ESTs
41324	6	R38904	Hs.13434	Homo sapiens clone 24418 mRNA sequence
18418	6	AA220086	Hs.60490	ESTs
23922	6	T84046	Hs.15345	ESTs
15342	6	W25781	Hs.8136	Homo sapiens clone 23998 mRNA sequence
15246	6	W01094	Hs.64628	ESTs
2247	6	M10321	Hs.110902	VON WILLEBRAND FACTOR PRECURSOR
31905	6	N25243	Hs.35996	Homo sapiens CASK mRNA complete cds
3002	6	C06238	Hs.95665	Homo sapiens clone 24700 unknown mRNA partial cds
38540	6	AA559142	Hs.112509	EST
42622	6	W87801	Hs.108209	ESTs

FIGURE 7 (CONT.)

27508	6	AA460671	Hs.54837	ESTs
7293	6	AA085354	EST - AA085354	ESTs
27322	6	AA424325	Hs.40496	ESTs
5774	6	X54189	Hs.82285	Phosphorylcholine transferase phosphoribosylglycinamide synthetase phosphoribosylaminoimidazole synthetase
33469	6	W87454	Hs.58987	ESTs Highly similar to homogenisate 12-dioxygenase [H. sapiens]
40329	6	H97488	Hs.108002	Human N-ethylmaleimide-sensitive factor mRNA partial cds
28539	6	AA278946	Hs.88522	ESTs
23579	6	T81098	Hs.124065	ESTs
22435	6	R67705	Hs.28706	ESTs
19956	6	H80942	Hs.37445	ESTs
18607	6	F02345	Hs.21197	ESTs
18991	6	H02554	Hs.30323	ESTs
7810	6	AA248169	Hs.106709	ESTs Highly similar to LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR [Rattus norvegicus]
30810	6	N53419	Hs.47646	ESTs
17998	6	AA159606	Hs.72815	ESTs
28245	6	AA252527	Hs.87794	ESTs
13348	6	AA449267	Hs.17914	ESTs Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA SUBUNIT [Mus musculus]
15034	6	U43701	Hs.75403	60S RIBOSOMAL PROTEIN L23A
33802	6	Z41059	Hs.79248	ESTs
33394	6	V84432	Hs.58670	ESTs
31170	6	N64017	Hs.48911	ESTs
40828	6	N64144	Hs.102749	EST
1789	6	L13288	Hs.535	Solute carrier family 17 (sodium phosphate) member 2
17740	5	AA142822	Hs.9817	ESTs
9509	5	H88070	Hs.49683	ESTs
15540	5	V30985	Hs.7535	ESTs
27827	5	AA458676	Hs.42355	ESTs
30697	5	N51585	Hs.47049	ESTs
40289	5	H57387	Hs.109745	ESTs
18927	5	AA036779	Hs.61826	Homo sapiens clone 23528 mRNA sequence
20658	5	N62915	Hs.57872	ESTs Weakly similar to weakly similar to myosin heavy chain [C. elegans]
31809	5	N62722	Hs.44602	ESTs
14677	5	T03568	Hs.14653	Homo sapiens mRNA for KIAA0625 protein partial cds
31102	5	N63178	Hs.46728	ESTs
22638	5	R38421	EST - RC_R38421	ESTs
23238	5	AA046507	Hs.92924	ESTs
32145	5	R38910	Hs.56110	Homo sapiens clone 24503 mRNA sequence
27870	5	AA046525	Hs.10247	Activated leucocyte cell adhesion molecule
34509	5	AA032974	Hs.111394	ESTs
25522	5	H85336	Hs.50250	ESTs

FIGURE 7 (CONT.)

32159	5	R40974	Hs.124270	ESTs	
35492	5	AA400514	Hs.97505	ESTs	
37630	5	AA459649	Hs.99485	ESTs	
27103	5	AA040492	Hs.63461	ESTs Weakly similar to kynurenine/alpha-aminoacidate aminotransferase [R.norvegicus]	
17209	5	AA082533	EST - RC_AA082533	EST - RC_AA082533	
589	5	D50930	Hs.5084	Human mRNA for KIAA0140 gene complete cds	
17489	5	AA122394	Hs.70811	ESTs	
6253	5	X80878	Hs.95262	Human R kappa B mRNA complete cds	
5087	5	U77645	Hs.21254	Human hTRIP (hTRIP) mRNA complete cds	
23060	5	T33513	Hs.7147	ESTs	
28902	5	D50590	Hs.45247	ESTs	
33228	5	R76401	Hs.92262	ESTs	
33218	5	W70259	Hs.48623	ESTs	
28751	5	D45455	Hs.65524	ESTs	
21400	5	R19360	Hs.14851	ESTs	
15557	5	V38290	Hs.9115	ESTs	
12631	5	AA412293	Hs.21258	ESTs	
32282	5	R62579	Hs.62264	ESTs	
10416	5	A000809	Hs.37599	ESTs	
40308	5	H83306	Hs.32980	Human mRNA for BST-1 complete cds	
33220	5	A3343299	Hs.7509	ESTs	
23100	5	W70279	Hs.84811	ESTs Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]	
15333	5	T23867	Hs.7716	ESTs	
9331	5	V24154	Hs.9166	ESTs	
9010	5	AA412555	EST - AA412555		
4690	5	C01360	Hs.67364	Homo sapiens clone 23504 mRNA sequence	
25213	5	U53295	Hs.72383	Sorting matn 1	
25212	5	A038464	Hs.103543	Hemo sapiens clone 24505 mRNA sequence	
28708	5	A0389333	Hs.30944	Myelothic syncytome antigen B [human fetal brain mRNA 3477 nt]	
7435	5	D05539	Hs.80165	EST	
25538	5	A0894412	Hs.25236	ESTs	
271	5	A0895560	Hs.101442	ESTs Highly similar to ZINC FINGER PROTEIN 5 [Homo sapiens]	
5490	5	D14823	EST - D14823		
18612	5	X04571	Hs.2230	Epidermal growth factor	
23393	5	F10040	Hs.13251	ESTs	
23446	5	T62916	Hs.11110	ESTs Weakly similar to ZINC FINGER PROTEIN 42 [H.sapiens]	
35204	5	T62682	Hs.12507	ESTs	
31369	5	AA396155	Hs.97600	ESTs	
5244	5	N67598	Hs.139355	ESTs	
	5	U65992	Hs.87197	Human clone IMAGE:35527 unknown protein mRNA partial cds	

FIGURE 7 (CONT.)

20835	5	N69215	Hs.37456	ESTs	
16502	5	AA027059	Hs.61425	EST	
22691	5	T87693	Hs.16414	ESTs	
31842	5	N60168	Hs.54593	EST	
7845	5	AA249611	EST - AA249611		
29297	5	H65459	Hs.38323	ESTs	
7953	5	AA284403	Hs.74750	Homo sapiens mRNA for KIAA0554 protein partial cds	
36412	5	AA428464	Hs.98468	ESTs	
19357	5	H18929	EST - RC_H18929		
16259	5	AA016258	EST - RC_AA016258		
23312	5	AA047078	ESTs Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]		
27617	5	AA446114	Hs.55409	ESTs	
42432	5	W65403	Hs.107293	ESTs	
39432	5	AA466883	Hs.78672	Laminin alpha 4	
32215	5	R45175	Hs.117183	ESTs	
18214	5	U93553	Hs.91310	Human alpha-1-fetoprotein transcription factor (HFTF) mRNA complete cds	
15141	5	U78798	Hs.90957	Human TNF receptor associated factor 6 (TRAF6) mRNA complete cds	
20052	5	H97822	Hs.5375	Human LAR-intracellular protein 1a mRNA complete cds	
7951	5	AA156838	Hs.107041	ESTs	
26451	5	AA250068	Hs.43616	ESTs	
42355	5	W20404	Hs.55405	ESTs	
39480	5	D90419	Hs.81915	STATHMIN	
17969	5	AA101633	Hs.89293	EST	
14693	5	U22172	Hs.73046	Human DNA damage repair and recombination protein RAD52 pseudogene mRNA partial cds	
22400	5	TS3336	Hs.105095	ESTs	
21153	5	R04315	EST - RC_R05315		
14282	5	AA505141	Hs.11923	ESTs	
21104	5	R01081	EST - RC_R01081		
32825	5	W20384	Hs.55412	ESTs	
35018	5	AA345691	EST - RC_AA349591		
25104	5	AA019598	Hs.103351	ESTs	
19235	5	H17225	Hs.31181	ESTs	
34979	5	AA347209	Hs.7941	Human mRNA for KIAA0324 gene partial cds	
21501	5	R26555	Hs.24120	ESTs	
18301	5	AA318543	Hs.10881	Homo sapiens mRNA for KIAA0541 protein partial cds	
37529	5	AA465112	Hs.59410	ESTs	
15552	5	W26914	Hs.32596	ESTs Highly similar to PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION [Escherichia coli]	
18588	5	AA262316	Hs.100385	ESTs	
24950	5	H60865	Hs.111026	Phosphatidylinositol glycan class F	
37294	5	AA450127	Hs.110571	ESTs Highly similar to MTELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD119 [Mus musculus]	

FIGURE 7 (CONT.)

35170	5	AA397630	Hs.38347	ESTs Weakly similar to rtp-1 [H.sapiens]
23201	5	T40552	Hs.8279	ESTs
27012	5	AA398913	Hs.49231	ESTs
28767	5	D45608	Hs.03792	Surfactant pulmonary-associated protein D
17777	5	AA149634	Hs.02788	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
20568	5	NE8009	Hs.38218	ESTs
20356	5	N89453	Hs.27371	ESTs
23375	5	T59670	Hs.10615	EST
17030	5	AA070168	EST - RC_AA070168	EST
30752	5	N52340	Hs.116084	EST
25808	5	AA149226	Hs.95821	Human osteoclast stimulating factor mRNA complete cds
31345	5	N67258	Hs.50139	ESTs
30784	5	N52857	Hs.47558	ESTs
13707	5	AA460281	Hs.14687	ESTs
29199	5	H25761	Hs.57082	EST
39003	4	AA605920	Hs.112785	EST
41529	4	R54458	Hs.2699	Glypican 1
3151	4	M33652	Hs.53155	Properdin P factor complement
33134	4	W61264	Hs.57629	ESTs
29196	4	H24456	Hs.85063	Homo sapiens clone 24440 mRNA sequence
12853	4	AA425782	Hs.27973	ESTs
11949	4	AA279527	Hs.125035	ESTs
31925	4	N82924	Hs.125032	ESTs
32526	4	AA398428	Hs.97528	ESTs
39338	4	H27216	Hs.07635	ESTs
30796	4	N53046	Hs.91146	ESTs Moderately similar to IIII ALU SURFAMILY J WARNING ENTRY IIII [H.sapiens]
19464	4	H24456	Hs.32085	EST
42486	4	W68410	Hs.06857	Calbindin 2 (28kD calsecalin)
34274	4	AA236332	Hs.10821	ESTs
37648	4	AA459917	Hs.99506	EST
3169	4	M85085	Hs.893	Cleavage stimulation factor 3' pre-RNA subunit 2 64KD
10326	4	R98417	Hs.107795	ESTs
15063	4	U98914	Hs.86648	Homo sapiens DNase gamma mRNA complete cds
23571	4	T00828	Hs.108169	ESTs
14377	4	AA509593	Hs.15299	ESTs Weakly similar to HSM-2 [H.sapiens]
22255	4	R95239	Hs.8956	ESTs
36820	4	AA435968	Hs.95449	ESTs Weakly similar to HSM-2 [H.sapiens]
35953	4	AA358015	Hs.99368	EST
12376	4	AA392271	Hs.19610	ESTs
31406	4	N68163	Hs.48405	EST

FIGURE 7 (CONT.)

27430	4	AA426028	Hs.42576	ESTs Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY IIII [H.sapiens]
30362	4	N01070	Hs.45046	ESTs
30559	4	N50039	Hs.47004	ESTs
27694	4	AA460319	Hs.48469	ESTs
31844	4	N60218	Hs.54607	ESTs
24635	4	AFFX.	AFFX-HUMGAPDHMB3197_M	
40506	4	N68829	Hs.131510	ESTs
35220	4	AA388246	Hs.97594	ESTs
10024	4	N94832	Hs.121699	ESTs
4238	4	U33053	Hs.24199	Human lipid-activated protein kinase PRK1 mRNA complete cds
26358	4	AA256398	Hs.88156	EST
24716	4	Z39734	Hs.22550	ESTs
19243	4	H13539	Hs.31222	ESTs
41844	4	T15833	Hs.100227	EST
38774	4	H17948	Hs.106311	Homo sapiens DGS-A mRNA 3' end
20111	4	N21380	Hs.25497	H.sapiens mRNA for ROX protein
24008	4	T93337	Hs.18624	ESTs
8316	4	AA410529	Hs.30732	ESTs
35072	4	AA358738	EST - RC, AA358738	
39784	4	H21819	Hs.14896	Homo sapiens clone 24590 mRNA sequence
1517	4	J04501	Hs.772	Glycogen synthase 1 (muscle)
9164	4	D38061	Hs.98807	Thrombosane A2 receptor
35027	4	AA349596	Hs.96937	ESTs
35185	4	AA389015	Hs.97590	ESTs
26570	4	AA279425	Hs.86428	ESTs Weakly similar to hypothetical L1 protein [H.sapiens]
15759	4	H4332	Hs.36873	ESTs
34310	4	AA243416	Hs.75470	Homo sapiens mRNA expressed in osteoblast complete cds
39981	4	H27317	Hs.108161	ESTs
23248	4	T47919	Hs.8749	ESTs
19119	4	H09077	Hs.30695	EST
14158	4	AA459182	Hs.118598	ESTs
22866	4	R59338	Hs.36189	EST
19335	4	AA059392	Hs.66791	ESTs
41950	4	T33137	Hs.7987	ESTs
20404	4	N46954	Hs.30881	Homo sapiens Igkn-alpha2 mRNA complete cds
18406	4	AA227962	Hs.112075	ESTs Weakly similar to reverse transcriptase [H.musculus]
15590	4	AA001908	Hs.24341	ESTs
28098	4	A242831	Hs.87606	ESTs
34360	4	AA251547	Hs.104358	EST
19830	4	AA054222	Hs.40400	ESTs

FIGURE 7 (CONT.)

32668	4	TE9264	Hs.2314	Mannose-binding lectin soluble (opsonic defect)
32912	4	W39051	EST - RC_W39051	
16230	4	AA011549	Hs.47884	ESTs
29696	4	H97903	Hs.42344	ESTs
8232	4	AA397929	EST - AA397529	
25584	4	AA112320	Hs.16704	ESTs
30878	4	N56882	Hs.46761	EST
40579	4	N34524	Hs.102516	ESTs
8026	4	AA301842	Hs.105169	ESTs Visually similar to reverse transcriptase homolog [H. sapiens]
3064	4	M77481	Human antigen (MAGE-1) gene complete cds	
17480	4	AA121974	Hs.72879	EST - RC_AA121974
15766	4	W95777	Hs.90804	ESTs
34865	4	AA299803	Hs.111458	EST
29779	4	N20290	Hs.42836	ESTs
9547	4	X55008	Hs.9568	Human mRNA for KIAA0385 gene complete cds
24479	4	W96222	Hs.34192	ESTs
16135	4	AA004805	Hs.63668	Human
11098	4	AA151243	Hs.39163	Toll-like receptor 2 (TLR2) mRNA complete cds
14388	4	AA399742	Hs.21600	ESTs
39078	4	AA417275	Hs.96214	ESTs
23440	4	T65966	Hs.12859	ESTs
20863	4	N99889	Hs.19167	ESTs
20347	4	N39117	Hs.12250	ESTs
10729	4	AA247455	Hs.15220	ESTs
20863	4	AA564087	Hs.18658	ESTs
12734	4	AA419200	Hs.5737	ESTs
24446	4	W93119	Hs.19512	ESTs
30734	4	N62083	Hs.47416	EST
25841	4	N62363	Hs.109695	ESTs
21183	4	R05769	Hs.19795	ESTs
18138	4	AA102757	Hs.131687	ESTs
35310	4	AA398682	Hs.37302	ESTs
29865	4	D00164	Hs.55340	ESTs
39407	4	N23343	Hs.43145	ESTs
8707	4	AA473685	Hs.79582	Homo sapiens mRNA for KIAA0593 protein partial cds
16472	4	AA233295	Hs.72156	ESTs
24720	4	Z39754	Hs.23235	ESTs
40825	4	N63823	Hs.102745	ESTs
13375	4	W63895	Hs.59876	ESTs
32669	4	W95211	Hs.54801	ESTs

FIGURE 7 (CONT.)

4	4641	U52426	Hs.74587	Homo sapiens COK (STIM1) mRNA complete cds
4	11796	AA225616	Hs.31707	ESTs
4	21571	R33941	Hs.24709	ESTs Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]
4	1800	K03474	EST - K03474	ESTs
4	21103	R01068	Hs.14603	ESTs
4	22953	T16358	Hs.105443	ESTs
4	39666	AA599661	Hs.106443	ESTs
4	27148	AA046231	Hs.100113	Human mRNA for KIA0381 gene partial cds
4	28580	D20261	Hs.80057	ESTs
4	36397	AA428372	Hs.105904	EST - RC_AA330634
4	28915	AA330634	EST - RC_AA330634	Human mRNA for histone H1x complete cds
4	6912	Z33278	Hs.2536	H-sapiens PEBP2aC1 acute myeloid leukaemia mRNA
4	31825	N85846	Hs.54543	ESTs
4	10763	AA057620	Hs.30007	ESTs
4	17007	AA069696	Hs.67317	ESTs
4	33439	W66445	Hs.59844	ESTs
4	27657	AA447612	Hs.60435	ESTs
4	26288	AA233393	Hs.87734	ESTs
4	8235	AA367616	Hs.107245	ESTs Moderately similar to potassium channel protein Raw3 [R.norvegicus]
4	12114	AA287057	Hs.25114	ESTs
4	879	D86155	Hs.97198	Human steroidogenic factor 1 mRNA complete cds
4	30793	N52979	Hs.51919	Plasminogen-like protein
4	13522	AA454115	Hs.6000	ESTs
4	20819	N89730	Hs.12160	ESTs
4	20019	H94266	Hs.9451	ESTs
4	32396	R95778	Hs.93008	EST
4	39162	AA487165	Hs.105706	EST
4	8487	AA442689	EST - AA442689	ESTs
4	18444	AA223848	Hs.69061	ESTs
4	16183	AA010070	Hs.80339	ESTs
4	33047	W49755	Hs.89589	ESTs Moderately similar to type Ia hair keratin a3 [H.sapiens]
4	14757	S82769	Hs.104133	GABAA receptor gamma 3 subunit [human fetal brain mRNA Partial 1536 nt]
3	26107	AA243172	Hs.87619	ESTs
3	24421	W52001	Hs.120969	ESTs
3	27655	AA447759	Hs.134724	ESTs
3	19154	H10047	Hs.22515	ESTs
3	10933	AA121360	Hs.27567	ESTs Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1 2-N-acetylglucosaminyltransferase [C.elegans]
3	7254	A074827	EST - A074827	ESTs
3	18684	R02952	Hs.22137	ESTs
3	40997	N77004	Hs.44380	ESTs

FIGURE 7 (CONT.)

14971	3	U1643	Human Mox1 protein (MOX1) mRNA complete cds
11217	3	Hs.439	ESTs
16752	3	AA180487	Hs.62460
21477	3	AA047365	Hs.82952 Homo sapiens mRNA for osteoblast specific cysteine-rich protein complete cds
21392	3	R20534	ESTs
11058	3	R18886	Hs.23631
30391	3	H28596	PROTEIN KINASE C THETA TYPE
21653	3	R30374	EST - RC142865
6102	3	R33005	Hs.23153 5-HYDROXYTRYPTAMINE 2B RECEPTOR
23602	3	X70340	ESTs Weakly similar to ETX1 (alternatively spliced) [H.sapiens]
6333	3	T70580	Transforming growth factor alpha
30500	3	AA412620	ESTs
21431	3	N45329	Hs.4248
39520	3	R22057	Hs.30490 ESTs Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F0938.3 IN CHROMOSOME III [Caenorhabditis elegans]
12065	3	AA412290	Hs.23336
19156	3	AA283307	Hs.98124
24844	3	H10088	Hs.110450 Homo sapiens clone 23837 mRNA sequence
33178	3	Z41301	Hs.25924 Homo sapiens clone 24486 mRNA sequence
2052	3	W68846	Hs.23539
15327	3	L38518	Hs.141719
18874	3	W23474	EST
9039	3	F10565	Hs.75339 Inositol polyphosphate phosphatase-like protein 1 (51C protein)
19167	3	CO2049	Hs.23352
34888	3	AA454935	Hs.12345
30591	3	H10641	Hs.106291
28997	3	AA303078	Hs.99566
18547	3	N49652	Hs.22928
17967	3	F03004	Hs.94479 Human G1334 protein (G1334) gene mRNA complete cds
15280	3	AA386486	Hs.138717
11047	3	W07019	Hs.93060
20465	3	N51599	Hs.27109
19451	3	AA142849	Hs.72163
41621	3	H23747	Hs.35088
2822	3	R59233	Hs.14633
28675	3	D20188	Hs.22660
13828	3	AA478441	Hs.31697
29473	3	H83694	Hs.101504
25829	3	AA151621	Hs.117946 N-acetylglucosaminyltransferase I
28532	3	C20680	Hs.74876
			Hs.11590
			Hs.40478
			Hs.110954
			Hs.68513

FIGURE 7 (CONT.)

32376	3	R91391	Hs.64391	ESTs	
12064	3	AA263848	Hs.11367	ESTs	Weakly similar to KIAA0009 [H.sapiens]
15547	3	W32012	Hs.23553	ESTs	
40284	3	H68073	Hs.108734	ESTs	Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PESA INTERGENIC REGION [Saccharomyces cerevisiae]
22861	3	R96955	Hs.38152	ESTs	
15525	3	W29763	Hs.16349	ESTs	
17668	3	AA167496	Hs.72869	EST	Homo sapiens KIAA0431 mRNA partial cds
3636	3	U12707	Hs.2157	EST	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)
4528	3	U42551	Hs.75871	EST	Homo sapiens protein kinase C-binding protein BACK7 mRNA partial cds
29784	3	N20468	Hs.42649	EST	ESTs Weakly similar to linc-1 protein ORF2 [H.sapiens]
7852	3	AA262100	EST	EST - AA262100	
15279	3	W05746	Hs.133202	ESTs	
42064	3	T63354	Hs.9225	ESTs	Highly similar to FIBRINOGEN-LIKE PROTEIN A PRECURSOR [Parasichthys parvimanatus]
17943	3	AA165147	Hs.20509	ESTs	
4506	3	U59743	Hs.19520	ESTs	Sodium/potassium ATPase gamma subunit
19421	3	AA022541	Hs.81146	ESTs	
4914	3	U67611	EST	EST - U67611	
39171	3	AA487301	Hs.105713	EST	
20168	3	N24106	Hs.27362	ESTs	Cellulose binding protein 1
19791	3	F08892	Hs.13575	ESTs	
24281	3	W70770	Hs.16371	ESTs	
13966	3	AA469507	Hs.15769	ESTs	
20583	3	N57797	Hs.34421	ESTs	
37181	3	AA448158	Hs.95152	EST	
21450	3	R23146	Hs.20468	ESTs	
19834	3	H44856	Hs.31697	ESTs	
10163	3	R54534	Hs.7688	ESTs	Homo sapiens clone 23338 mRNA sequence
7055	3	Z56810	EST	EST - Z56810	
25782	3	AA138588	Hs.91797	ESTs	Reinoblastoma-binding protein (alternative products)
27456	3	AA426500	Hs.32597	ESTs	
25023	3	F09302	EST	EST - RC_F09302	
10569	3	AA113266	Hs.8023	ESTs	Homo sapiens mRNA for SPQP
6357	3	X57746	EST	EST - X57748	
8722	3	AA481309	Hs.30204	ESTs	
21476	3	R23065	Hs.23523	ESTs	
14086	3	AA487558	Hs.8135	ESTs	
35382	3	AA389562	Hs.97566	ESTs	
28608	3	C21509	Hs.112774	ESTs	
13350	3	AA449297	ESTs	ESTs Weakly similar to type 1 procollagen C-proteinase enhancer protein precursor [H.sapiens]	
41202	3	R12808	Hs.113619	ESTs	

FIGURE 7 (CONT.)

15912	3	W51985	Hs.73372	ESTs	
33930	3	AA1195339	Hs.95870	ESTs	
34215	3	AA233855	Hs.104252	UTROPHIN	
19208	3	H11724	Hs.110454	ESTs Weakly similar to coded for by C. elegans cDNA cm10a3 [C.elegans]	
24047	3	W15396	Hs.26750	ESTs	
14852	3	T52099	Hs.100383	ESTs Highly similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOPLASMIC [Rattus norvegicus]	
27615	3	AA485370	Hs.59729	ESTs	
22610	3	R81173	Hs.11482	ESTs Highly similar to F11 antigen [H.sapiens]	
37510	3	AA455996	Hs.2999	Glykcan 1	
37825	3	AA470073	Hs.104836	ESTs	
13321	3	AA448238	Hs.16714	ESTs	
29599	3	AA235375	Hs.87421	EST	
9738	3	M13150	Hs.96900	MAS1 oncogene	
16248	3	AA013125	Hs.40871	ESTs	
27592	3	AA442896	Hs.61979	ESTs Moderately similar to THREONYL-TRNA SYNTHETASE CYTOPLASMIC [H.sapiens]	
18546	3	AA029452	Hs.95162	ESTs	
16681	3	AA084659	EST - RC_AA084659	Homo sapiens retinoid acid hydroxylase mRNA complete cds	
22128	3	R51021	Hs.23161	EST - RC_T54617	
23312	3	T54617	Hs.124205	ESTs	
18783	3	F09741	Hs.127585	ESTs	
10308	3	R86920	Hs.23996	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]	
22518	3	R71892	Hs.25024	ESTs Weakly similar to estrogen-responsive finger protein efp [H.sapiens]	
8285	3	AA400226	Hs.40550	ESTs Moderately similar to proto-cadherin 3 [R.norvegicus]	
16391	3	AA019218	Hs.2037	Tumor necrosis factor	
5453	3	X02910	Hs.29190	ESTs	
22509	3	R71393	Hs.27291	ESTs	
20065	3	H98657	Hs.138746	EST	
31091	3	N63076	Hs.124849	ESTs	
39050	3	AA510112	Hs.77385	MYOSIN LIGHT CHAIN ALKALI SMOOTH-MUSCLE ISOFORM	
2493	3	M22919	Hs.44069	ESTs	
30159	3	N32623	Hs.22583	ESTs Highly similar to co-repressor protein [M.musculis]	
28913	3	F01560	Hs.4221	ESTs	
12257	3	AA350030	Hs.75119	Human mRNA for type 2 inositol 145-phosphate receptor complete cds	
359	3	D26350	Hs.14906	ESTs	
23587	3	T81388	Hs.12851	ESTs	
14323	3	AA598575	Hs.7491	Homo sapiens methionine synthase reductase [MTRR] mRNA complete cds	
27231	3	AA416636	Hs.133096	ESTs	
34614	3	AA338729	Hs.19308	ESTs	
21233	3	R08359	Hs.19193	ESTs	
23650	3	T86475	Hs.19193	ESTs	

FIGURE 7 (CONT.)

14236	3	AA489891	Hs.5011	ESTs Weakly similar to The hst27 gene product is related to S.pombe rad21 gene product. [H.sapiens]
17617	3	AA131394	Hs.4472	ESTs Weakly similar to The KIA0147 gene product is related to adenyl cyclase. [H.sapiens]
24594	3	Z38804	Hs.2255	ESTs Highly similar to OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR [Bos laurus]
7426	3	AA086865	Hs.111818	Homo sapiens heat shock factor binding protein 1 HSBP1 mRNA complete cds
34871	3	AA300151	Hs.125146	ESTs
17962	3	AA167051	Hs.6325	Human brain mRNA homologous to 3'UTR of human CD24 gene partial sequence
24337	3	W66007	Hs.8876	ESTs
22569	3	R75950	Hs.29674	ESTs
24554	3	Z38522	Hs.27382	EST
22348	3	R81750	Hs.6136	ESTs
30217	3	N34288	Hs.44154	EST
10210	3	R57468	Hs.131828	ESTs
22156	3	R52145	Hs.25594	ESTs
18404	3	AA021294	Hs.60554	ESTs Moderately similar to sodium-calcium exchanger form 3 [R.novoglaui]
23310	3	H68642	Hs.88729	ESTs
15995	3	Z21217	Hs.77595	Human mRNA for KIA0008 gene complete cds
9758	3	M25393	Hs.127610	Acyl-Coenzyme A dehydrogenase C-2 to C-3 short chain
20817	3	N72395	Hs.18004	ESTs
4847	3	U64573	EST - U64573	
22694	3	T10362	Hs.57958	ESTs
9808	2	M75432	Hs.89633	Probable transcription factor PML (alternative products)
29607	2	N21031	Hs.42930	ESTs
39646	2	H02295	Hs.7268	Homo sapiens clone 23872 mRNA sequence
22733	2	R82181	Hs.34558	EST
23233	2	T41177	Hs.8410	Homo sapiens retinoic acid-inducible endogenous telomeric DNA
18549	2	F01350	Hs.6092	ESTs Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02E3.7 IN CHROMOSOME III [Caenorhabditis elegans]
31892	2	N91968	Hs.39535	ESTs
18991	2	F10452	Hs.12254	ESTs
24553	2	Z38521	Hs.9426	ESTs
16289	2	H16568	Hs.23748	ESTs
14185	2	AA450911	Hs.22393	Homo sapiens dpt1 mRNA complete cds
30723	2	N51935	Hs.47374	EST
34031	2	AA192014	Hs.83577	Human LIM protein MLP mRNA complete cds
18434	2	A4322206	Hs.50743	ESTs
14647	2	D20378	Hs.30731	EST
41048	2	N62734	Hs.115585	ESTs
38157	2	AA466858	Hs.103702	EST
32399	2	W77390	Hs.73903	MAIINGLOBULIN-RELATED 14.1 PROTEIN PRECURSOR
18616	2	AA035446	Hs.61783	ESTs
3276	2	M93716	Hs.76993	Nitic oxide synthase 3 (endothelial cell)

FIGURE 7 (CONT.)

33022	2	V446976	Hs.94667	EST	ESTs
31704	2	N73065	Hs.14632	ESTs	ESTs
39873	2	AA635077	Hs.112075	ESTs	ESTs
20396	2	N42693	Hs.12266	ESTs	ESTs
10310	2	R67373	Hs.75429	ESTs	ESTs
22358	2	R63655	Hs.1432	Protein Kinase C substrate SKK-H	
19596	2	T21737	Hs.2864	Flavin-containing monooxygenase 4	
23667	2	T69226	Hs.142628	ESTs	ESTs
39803	2	N57730	Hs.48058	EST	ESTs
20338	2	N73988	Hs.37477	CDW52 antigen (CAMPATH-1 antigen)	ESTs
5935	2	X62466	Hs.108338	ESTs	ESTs
19304	2	H16976	Hs.7973	ESTs	ESTs
8804	2	AB004463	Hs.16227	Homo sapiens mRNA for SH3 binding protein complete cds clone RES4-23A	
41485	2	R49689	Hs.5260	ESTs Weakly similar to O6659.3 [C.elegans]	
24685	2	Z39406	Hs.11797	ESTs Moderately similar to retinoid X receptor interacting protein [M.musculus]	
25403	2	AA063316		EST - RC_AA063316	
35773	2	AA406219	Hs.104747	ESTs	ESTs
27885	2	AA464267	Hs.24912	Homo sapiens bicaudal-D (BICD) mRNA complete cds	
16911	2	AA058659	Hs.60969	ESTs	ESTs
42315	2	T97353		EST - RC_T97353	
40632	2	N45221		EST - RC_N45221	
15722	2	W79046	Hs.15250	Homo sapiens DBI-related protein mRNA complete cds	
14842	2	T47519		EST - T47519	
38086	2	AA417344	Hs.99220	ESTs Moderately similar to located at OATL1 [H.sapiens]	
15527	2	W28786	Hs.63260	Phosphodiesterase 6A cAMP-specific rod alpha	
10302	2	R84933	Hs.133217	ESTs	ESTs
21243	2	R68773	Hs.20231	ESTs	ESTs
7759	2	AA234687	Hs.64147	ESTs Weakly similar to F59C5.4 [C.elegans]	
31672	2	N74336	Hs.91681	ESTs	ESTs
26769	2	AA284722	Hs.85121	ESTs	ESTs
23687	2	AA156504	Hs.95875	EST	ESTs
19685	2	AA043115	Hs.5452	ESTs Weakly similar to ORF YDL077c [S.cerevisiae]	
864	2	HG1804-		EST - HG1804-HT1829	
12439	2	AA401452	Hs.32060	ESTs	ESTs
19569	2	H41235	Hs.109668	ESTs	ESTs
24223	2	W70168	Hs.22696	ESTs	ESTs
21052	2	N63764	Hs.10175	ESTs Weakly similar to hypothetical protein [H.sapiens]	
17453	2	AA121336		EST - RC_AA121336	
28948	2	F03032	Hs.65826	ESTs Weakly similar to reverse transcriptase homolog [H.sapiens]	
34140	2	AA215537	Hs.104186	ESTs	ESTs

FIGURE 7 (CONT.)

7465	2	AA120886	EST - AA120886	
17376	2	AA102425	EST - RC_AA102425	
5130	2	U79288	Hs.0503	Homo sapiens clone 24440 mRNA sequence
30241	2	N27628	Hs.132744	Homo sapiens clone 24525 mRNA sequence
19834	2	H46488	Hs.143798	ESTs
8168	2	AA360963	EST - AA360963	
20202	2	H11595	Hs.22482	ESTs
20439	2	N50785	Hs.13269	ESTs
10431	2	AA011310	Hs.3757	ESTs
23707	2	H86244	Hs.42519	ESTs
38668	2	H37909	Hs.107950	ESTs
8868	2	C00155	Hs.10444	ESTs
41350	2	F40442	Hs.75952	Guanthione S-transferase M5
13121	2	AA436156	Hs.110337	ESTs
15747	2	F03989	Hs.132758	ESTs
18674	2	H51016	Hs.18995	ESTs Weakly similar to KIAA0412 [H-sapiens]
814	2	T91086	EST - RC_T91086	EST - HG1019-HT1019
23804	2	AA279089	Hs.86550	ESTs
26555	2	AA453381	Hs.104900	ESTs
6597	2	N47856	Hs.64607	Human RACH1 (RACH1) mRNA complete cds
30457	2	R45441	Hs.23710	ESTs
21975	2	AA120706	Hs.70724	ESTs
17452	2	N83495	Hs.54590	ESTs
31958	2	N89550	Hs.49759	ESTs
32490	2	T10389	Hs.81248	Human RNA-binding protein CUG-BP1/NBAB50 (NAB50) mRNA complete cds
39174	2	AA621087	Hs.112944	ESTs
21572	2	R34073	Hs.89740	Zinc finger protein 132 (clone pHZ-20)
15914	2	V05846	Hs.81972	V-aki avian sarcoma viral oncogene homolog
12014	2	AA281769	Hs.7214	Human HpaST (HpaST) mRNA complete cds
39777	2	H18412	Hs.75253	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA alternatively spliced partial cds
9484	2	H50178	Hs.100901	ESTs Highly similar to PROTEIN PHOSPHATASE PP2A 55 KD REGULATORY SUBUNIT NEURONAL ISOFORM (Nrcollagus culicoides)
19147	2	H09751	Hs.117619	ESTs
32778	2	AA424179	Hs.124027	ESTs
16475	2	AA025903	Hs.57911	ESTs
21304	2	R11208	Hs.20755	ESTs
11159	2	AA176448	Hs.10024	ESTs
18093	2	AA167985	Hs.85564	ESTs
19190	2	H11274	Hs.31040	EST
15710	2	W76399	EST - W76399	

FIGURE 7 (CONT.)

18707	2	FM627	Hs.2354.0	ESTs	
6477	2	X91504	Hs.64904	Transcription factor COUP-2 (a.k.a. ARP1)	
20923	2	N38869	Hs.15119	ESTs	
16338	2	A0018601	Hs.75649	EXTRACELLULAR SIGNAL-REGULATED KINASE 3	
19680	2	H48457	Hs.35104	ESTs	
24833	2	Z41087	Hs.19306	ESTs	
24038	2	W232709	Hs.108947	ESTs	
26180	2	A4351230	Hs.112272	ESTs	
37177	2	A4447386	Hs.7705	ESTs	
28190	2	A4462387	Hs.20054	ESTs	
10407	2	A4056653	Hs.22552	ESTs	
10770	2	T47001	Hs.138905	ESTs	
41894	2	H12243	EST - RC_A112243		
18217	2	A4428869	Acroisin		
36532	2	T60072	Hs.10666	ESTs	
23376	2	J03071	Hs.115352	Growth hormone 1	
1450	2	2	ESTs Moderately similar to IIII ALU CLASS B WARNING ENTRY IIII [H-sapiens]		
9007	2	A4230072	Hs.97263	EST - RC_A0094723	
12665	2	A4094723	ESTs		
24619	2	240923	Hs.24612	ESTs	
5532	2	X93525	Hs.69491	DNA-BINDING PROTEIN A	
26550	2	A4297851	Hs.86641	ESTs	
34175	2	A4227523	Hs.103788	ESTs	
34620	2	A4282169	EST - RC_A0382169		
27065	2	A4402465	Hs.77978	ESTs	
20173	2	N24730	Hs.15420	ESTs	
17574	2	A4126060	EST - RC_A4126060		
22330	2	R60520	Hs.28419	Homo sapiens clone 24510 mRNA sequence	
30070	2	N29698	Hs.44076	EST	
20487	2	N52322	Hs.19878	ESTs	
724	2	D83703	Hs.30729	Peroxisomal biogenesis factor 6	
4132	2	U27655	Hs.87254	Human RGP3 mRNA complete cds	
8557	2	A4452705	Hs.23954	ESTs Weakly similar to D2045.9 [C.elegans]	
33659	2	W89526	Hs.59718	EST	
13375	2	A4449716	Hs.5723	ESTs	
30891	2	N57007	Hs.94074	EST	
13988	2	A4460045	Hs.7934	ESTs	
22306	2	R59008	Hs.109530	ESTs	
23167	2	T33164	Hs.12840	Homo sapiens germline mRNA sequence	
20673	2	N70134	Hs.31476	ESTs	
7231	2	A4059327	Hs.6580	Homo sapiens clone 23718 mRNA sequence	

FIGURE 7 (CONT.)

24562	2	Z39752	Hs.26330	ESTs	
11320	2	AA213067	Hs.22222	ESTs	
16388	2	AA020781	Hs.60847	ESTs	
24608	2	Z39888	Hs.25046	ESTs	
7809	2	AA248065	Hs.12469	Homo sapiens clone 23930 mRNA sequence	
13163	2	AA437225	Hs.22410	ESTs	
20549	2	N54991	Hs.37591	ESTs	ESTs Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]
1139	2	H63227		EST - HG3227-HT3404	
35572	2	AA401489		EST - RC_AA401489	
6964	2	Z49105	Hs.137591	H.sapiens HD21 mRNA	
27704	2	AA449704	Hs.77637	Homo box A4	
33196	2	W69725	Hs.10711	ESTs	
30963	2	N53373	Hs.28912	ESTs	
13886	2	AA476937	Hs.24441	ESTs	
18164	2	AA007509	Hs.75395	Human mRNA for TPRD complete cds	
18083	2	AA181826	Hs.70564	Homo sapiens mRNA for hoxA7 protein	
20107	2	N21207	Hs.129942	ESTs Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]	
23004	2	T16556	Hs.6653	ESTs	
16238	2	AA011678	Hs.40470	ESTs	
18189	2	AA195042	Hs.85978	ESTs	
37567	2	AA457377		EST - RC_AA457377	
2174	2	L42611	Hs.11758	KERATIN TYPE II CYTOSKELETAL GD	
38958	2	AA009707	Hs.12751	ESTs	
37919	2	AA478162	Hs.104965	ESTs	
28905	2	D81123	Hs.57475	ESTs	
33315	2	W74418	Hs.55410	ESTs	
7421	2	AA065600		EST - AA065600	
3745	2	U09117	Hs.80776	Human phospholipase c delta 1 mRNA complete cds	
19545	2	H37834	Hs.32569	ESTs	
21204	2	R07632	Hs.17549	ESTs	
8416	2	AA428531		EST - AA428531	
17569	2	AA128926		EST - RC_AA128926	
15672	2	H38195	Hs.22223	ESTs	
22760	2	R35714	Hs.33633	ESTs	ESTs Highly similar to ALPHA-2-MACROGLOBULIN PRECURSOR [Homo sapiens]
19354	2	H18829	Hs.121515	ESTs	
40618	2	N38565	Hs.108540	ESTs	
29973	2	N23708	Hs.43429	ESTs	
22571	2	R78565	Hs.136395	EST	
7698	2	AA174185	Hs.3354	Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA complete cds	
25395	2	AA059089	Hs.109727	ESTs	

FIGURE 7 (CONT.)

14176	2	AA490620	Hs.11809	ESTs	
37400	2	AA453578	Hs.120994	ESTs	Weakly similar to T20D3.5 [C.elegans]
29467	2	H85120	Hs.80881	N-ACETYL-LACTOSAMINE SYNTHASE	
10197	2	D61199	Hs.50785	Homo sapiens vesicle trafficking protein sec22b mRNA complete cds	
322	2	D21241	EST - D21241_xpt1		
22224	2	R55192	Hs.25689	ESTs	
19488	2	H27675	Hs.25604	ESTs	
10568	2	AA029703	Hs.36574	ESTs	
10872	2	AA099557	Hs.15780	ESTs	Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]
29687	2	N26172	Hs.43760	ESTs	
30739	2	N53143	Hs.64001	ESTs	
9638	2	L07592	Hs.106415	Human peroxisome proliferator activated receptor mRNA complete cds	
21059	2	N99461	Hs.17706	ESTs	
27195	2	AA411473	Hs.65311	ESTs	
9241	2	D79565	EST - D79565		
9218	2	D61469	Hs.56896	ESTs	
22238	2	R55763	Hs.107287	ESTs	
7512	2	AA136369	EST - AA136369		
17438	2	AA115508	Hs.2780	Jun D proto-oncogene	
24932	2	AFFX-	AFFX-HSAC07/X00351_M		
28911	2	F01525	Hs.3786	Glutamate receptor metabotropic 3	
10944	2	AA125969	Hs.34769	ESTs	Weakly similar to F35G12.9 [C.elegans]
42324	2	T81199	Hs.142702	ESTs	
34756	2	AA287665	Hs.5245	ESTs	
12743	2	AA421050	Hs.24545	ESTs	
21275	2	R10075	Hs.14860	ESTs	
13876	2	AA459389	Hs.29350	Homo sapiens mRNA for lysosyl sulfoltransferase-2	
13009	2	AA430474	Hs.15466	ESTs	
7403	2	AA094921	Hs.79768	ESTs	
11151	2	AA150861	Hs.25819	ESTs	
35669	2	AA404707	Hs.54865	ESTs	
17701	2	AA135941	Hs.71626	ESTs	
18713	2	F04696	Hs.21782	ESTs	
24144	2	V02312	Hs.30303	ESTs	Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]
30741	2	N52175	Hs.22222	ESTs	
23042	2	T23433	Hs.7105	ESTs	
18479	2	AA233483	Hs.87159	ESTs	
5314	2	AA410355	ESTs	Highly similar to RIBOSOMAL PROTEIN S6 KINASE [Homo sapiens]	
7690	2	AA291786	Hs.103081	ESTs	Weakly similar to HYPOTHETICAL PROTEIN KIAU168 [H.sapiens]
10388	2	AA053555	EST - RC_AA053555		

FIGURE 7 (CONT.)

9407	2	H20086	EST - H20086	
42791	2	AFFX-	AFFX-HUMGAPDH33197_M	
28302	2	AA255470	ESTs	
30722	1	N51924	ESTs	
24965	1	AFFX-	AFFX-Lyx-5	
38850	1	AA609262	EST - RC_AA609262	
13746	1	AA461300	ESTs	
6963	1	Z30643	Hs.123123 H.sapiens mRNA for chloride channel (putative) 2138bp	
31403	1	N68117	Hs.41119 ESTs	
17630	1	AA152312	Hs.72047 ESTs	
10583	1	AA033874	Hs.12035 ESTs	
20913	1	N72116	Hs.57435 Natural resistance-associated macrophage protein 2	
35507	1	AA402267	Hs.133475 ESTs Weakly similar to zinc finger protein [H.sapiens]	
9920	1	N44756	Hs.141935 ESTs Weakly similar to transformilin-related protein [H.sapiens]	
9468	1	H48074	Hs.31552 ESTs	
29459	1	H62529	EST - RC_H62529	
18121	1	AA181310	Protein phosphatase 2 (formerly 2A) regulatory subunit A (PR 65) beta isoform	
14705	1	D59382	EST - RC_D59382	
16592	1	F04444	ESTs	
16543	1	AA029430	Hs.6217 ESTs	
16359	1	AA019197	Hs.61557 EST	
40818	1	N63772	Hs.144550 Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrog	
35205	1	AA388161	Hs.97902 ESTs	
7831	1	AA249176	Hs.68334 ESTs	
17794	1	AA150280	Hs.72062 ESTs	
11347	1	AA224245	Hs.26912 ESTs	
17919	1	AA181125	Hs.72384 EST	
22184	1	R33520	Hs.102755 ESTs	
14827	1	T32288	Hs.60421 ESTs	
28091	1	AA481768	Hs.87593 ESTs	
28815	1	D59267	Hs.56762 ESTs	
17813	1	AA151480	Hs.91202 ESTs	
24655	1	Z39191	Hs.27262 ESTs Weakly similar to Lpt17p [S.cerevisiae]	
19511	1	W51743	Hs.35096 ESTs	
39696	1	H82865	Hs.38132 ESTs	
15700	1	W73559	Hs.75051 EST	
22045	1	R46965	Hs.24796 EST	
38770	1	AA435753	Homo sapiens mesoderm-specific basic-helix-loop-helix protein (POD1) mRNA complete cds	
9877	1	N31127	EST - RC_AA435753	
22487	1	R82284	Hs.40098 ESTs	
			Hs.26399 ESTs	

FIGURE 7 (CONT.)

32410	1	R07176	Hs.110763	ESTs	
18002	1	A0694425	Hs.20573	ESTs	
23033	1	T11353	Homo sapiens clone 23018 mRNA sequence		
17593	1	A4129866	EST - RC_AA129866		
14887	1	T55688	Hs.100419	ESTs	
20286	1	I32118	Hs.107385	ESTs Highly similar to THREONYL-TRNA SYNTHETASE CYTOSOLIC [Homo sapiens]	
14447	1	A4680045	Hs.11759	ESTs	
37994	1	A4179919	EST - RC_AA417919		
12882	1	A4425221	Hs.18528	Homo sapiens mRNA for N414 protein	
11970	1	A4260667	Hs.4069	ESTs	
19738	1	H53059	Hs.15540	ESTs	
14471	1	A4693546	Hs.20102	ESTs	
14855	1	T34762	Hs.9786	ESTs	
24725	1	Z39761	Hs.36975	Cholinergic receptor nicotinic delta polypeptide	
5796	1	X55019	Hs.3004	Homo sapiens Duo mRNA complete cds	
20259	1	N31598	Hs.12727	ESTs	
18441	1	A4325208	Hs.77480	ESTs	
19488	1	A4233177	Hs.87134	ESTs	
10164	1	R54743	Hs.19400	ESTs Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]	
8830	1	A9023219	Hs.8563	Human mRNA for KIAA0321 gene partial cds	
15297	1	V07491	Hs.121559	ESTs Highly similar to DIPHTHINE SYNTHASE [Saccharomyces cerevisiae]	
16477	1	A4026031	Hs.61312	ESTs	
21969	1	R45334	Hs.21175	ESTs	
22340	1	R61522	Hs.26892	ESTs	
12854	1	A4426259	EST - RC_AA426259		
8692	1	A4477891	Hs.104476	ESTs	
22594	1	R79793	Hs.23900	ESTs	
19131	1	H09331	Hs.122791	ESTs	
17103	1	AA074997	EST - RC_AA074997		
35920	1	A4402493	Hs.10552	ESTs Highly similar to c-Jun leucine zipper interactive [M.musculus]	
35401	1	A4399593	Hs.97662	EST	
10991	1	AA112307	Hs.25224	ESTs	
19546	1	H76901	Hs.32706	ESTs	
18378	1	V26448	Hs.15071	ESTs Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]	
30262	1	N35978	Hs.82354	ESTs	
39057	1	AA620607	Hs.111591	ESTs	
37896	1	AA477463	Hs.77039	Ribosomal protein S28	
8836	1	AB002325	Hs.105917	Human mRNA for KIAA0327 protein complete cds	
16150	1	AA005428	Hs.60140	ESTs	
23955	1	T97457	Hs.15065	ESTs Weakly similar to alternatively spliced product using exon 13A [H.sapiens]	

FIGURE 7 (CONT.)

37812	AA469639	Hs.105323	ESTs	
14762	S72370	Hs.89890	Pyruvate carboxylase	
23540	T79178	Hs.14463	ESTs	
41552	R93952	Hs.101253	Human mRNA for KIAA0296 gene complete cds	
21935	R42569	Hs.22444	EST	
11467	AA234089	Hs.14593	ESTs	
18347	AA219230	Hs.86815	ESTs	
8215	AA389673	Hs.61344	ESTs Weakly similar to No definition line found [C.elegans]	
15505	W28396	Hs.7252	Human sapiens clone 24800 mRNA sequence	
22764	R93802	Hs.33687	ESTs	
14966	U07620	Hs.89681	Human MAP kinase mRNA complete cds	
24213	W59164	Hs.23973	ESTs	
8165	AA358868	Hs.104135	Human sapiens mRNA for DRIM protein	
32724	T80750	Hs.15230	ESTs Weakly similar to F25H2.2 [C.elegans]	
8212	AA386236	Hs.30757	Human sapiens transcription factor SUPT3H (SUPT3H) mRNA complete cds	
9834	M62259	Hs.22554	Homo sapiens B5 (2.1 protein)	
7229	AA059213	Hs.91898	ESTs	
15649	W58725	Hs.75074	H. sapiens mRNA for MAP kinase activated protein kinase	
42306	T96538	Hs.15090	Human K ⁺ channel beta 1a subunit mRNA alternatively spliced complete cds	
9159	D31483	Hs.30062	Human sapiens clone 23565 unknown mRNA partial cds	
20040	H96712	Hs.125198	ESTs	
42218	T86444	Hs.110095	ESTs	
15526	W28790	Hs.8124	ESTs	
17790	AA150192	Hs.42262	ESTs Weakly similar to HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III [C.elegans]	
17595	AA125929	Hs.71166	EST	
31314	N68805	Hs.49278	EST	
9777	M57888	Hs.95946	GRANZYME H PRECURSOR	
15373	W26376	Hs.74583	THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR	
23547	T79448	Hs.14577	EST	
12076	AA284362	Hs.6448	ESTs Weakly similar to No definition line found [C.elegans]	
11956	AA279991	Hs.12491	ESTs	
15391	W28651	Hs.15961	ESTs	
9287	D92257	Hs.19104	ESTs	
16419	AA022466	Hs.81141	EST	
21713	R39930	Hs.21034	ESTs	
12905	AA427537	Hs.32419	ESTs	
30257	N34561	Hs.75873	H. sapiens mRNA for Zyxin	
28134	AA487522	Hs.64065	ESTs	
16380	AA019750	Hs.40797	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	
10553	AA028904	Hs.33215	ESTs	

FIGURE 7 (CONT.)

18063	1	AA180054	Hs.73577	ESTs	
39820	1	H24085	Hs.25443	ESTs	
7374	1	AA093378	Hs.101810	ESTs	
13109	1	AA435638	Hs.7985	ESTs	
19370	1	H19873	Hs.31670	ESTs	
24325	1	W84733	Hs.3078	ESTs	
22318	1	R60224	Hs.7065	ESTs	
24249	1	V73069	Hs.12600	ESTs	
16514	1	AA427846	Hs.44608	ESTs	
21421	1	R21741	Hs.23258	EST	
8397	1	AA426178	Hs.71725	ESTs	Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]
8412	1	AA428090	Hs.25102	ESTs	
10072	1	R14782	Hs.31931	ESTs	
10349	1	AA001908	Hs.18100	ESTs	
14492	1	AA609535	Hs.27497	ESTs	
14930	1	T92512		EST - T92512	
15861	1	X81001	Hs.41503	Small inducible cytokine A5 (RANTES)	
16705	1	AA043800	Hs.62245	ESTs	
16744	1	AA045543	Hs.62866	EST	
16950	1	AA082380	Hs.65860	ESTs	
17835	1	AA158779	Hs.29759	ESTs	Weakly similar to IIII ALU SUBFAMILY SX WARNING ENTRY IIII [H.sapiens]
18834	1	F10207	Hs.13269	ESTs	
19178	1	H10992	Hs.100910	EST	
19767	1	H54720	Hs.36841	ESTs	
21341	1	R14959	Hs.21871	EST	Moderately similar to ninein [M.musculus]
21466	1	R24518	Hs.23674	EST	
21602	1	R36524	Hs.135137	ESTs	
21748	1	R40697	Hs.21290	EST	
21860	1	R43089		EST - RC_R43089	
21891	1	R43590	Hs.13290	ESTs	
21937	1	R44508	Hs.22653	ESTs	
22006	1	R45244	Hs.23110	ESTs	
22054	1	R48116	Hs.25067	EST	
22222	1	R55042	Hs.106645	ESTs	
22292	1	R55385	Hs.141053	Homo sapiens testophilin (VMD2) mRNA alternatively spliced product complete cds	
22393	1	R63463	Hs.23282	ESTs	
22446	1	R67259	Hs.25969	EST	
23103	1	T23839	Hs.7344	ESTs	
23872	1	T94592	Hs.17338	EST	
24291	1	W80842	Hs.16961	ESTs	

FIGURE 7 (CONT.)

24640	1	Z35086	Hs.21403	ESTs	
27519	1	AA439535	Hs.50695	ESTs	
32067	1	R06424	Hs.61896	ESTs	
32204	1	R44210	Hs.91440	EST	
32862	1	T75842	Hs.90830	ESTs	
33714	1	Z38430	Hs.65749	ESTs	
33733	1	Z39568	Hs.65792	ESTs	
33873	1	AFFX	AFFX.Dap.X.3		
33434	1	A4400034	Hs.97769	EST	
35950	1	A4412498	Hs.104778	ESTs	
36483	1	A4428865	Hs.95563	ESTs	
36515	1	A4431469	Hs.89737	ESTs	
37326	1	AA452198	Hs.37391	Homo sapiens BAC clone RG118D07 from Tq31	
37706	1	AA461090	Hs.24626	EST	
38285	1	AA485940	Hs.165302	ESTs	
38887	1	AA608402	Hs.12705	EST	
38933	1	AA608656	Hs.12702	ESTs	
38994	1	A490317	Hs.14150	ESTs	
40244	1	H51887	Hs.10250	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA complete cds	
40845	1	N47852	Hs.109304	ESTs	
40945	1	N63793	Hs.109304	ESTs	
43918	1	R44911	Hs.137686	ESTs Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	
44165	1	R33829	Hs.101953	EST	
44700	1	T03110	Hs.100165	EST	
47776	1	AA465807	Hs.0775	ESTs Highly similar to ALANINE AMINOTRANSFERASE [Homo sapiens]	
13264	1	A4302708	Hs.3009	ESTs Weakly similar to MTERP [H.sapiens]	
8171	1	AA046650	Hs.40342	ESTs	
23030	1	T17291	Hs.5995	ESTs	
8406	1	AA427510	Hs.104267	ESTs	
10707	1	AA046650	Hs.40342	ESTs	
23010	1	AA005315	Hs.51262	ESTs	
14829	1	T35529	EST - T35529		
34584	1	AA209354	Hs.132872	ESTs Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII [H.sapiens]	
15902	1	T07668	Hs.38942	H.sapiens mRNA for Plp1 isolate 1	
9622	1	N44971	Hs.107154	Spectrin beta non-erythrocytic 1	
13381	1	V21436	Hs.107725	ESTs Weakly similar to LIS-1 protein [H.sapiens]	
22168	1	R53024	Hs.25985	ESTs	
11690	1	AA252762	Hs.31235	ESTs	
22959	1	T16510	Hs.6624	ESTs	
24490	1	Z38153	Hs.26921	ESTs	
19950	1	H91255	Hs.15227	ESTs	

FIGURE 7 (CONT.)

19689	1	H48825	Hs.38291	ESTs
12450	1	AA01809	Hs.19865	ESTs
24368	1	W87280	Hs.124800	ESTs
22565	1	R77631	Hs.29126	ESTs
18872	1	F10542	Hs.12292	ESTs
15358	1	W61105	Hs.8961	ESTs
24186	1	W61319	Hs.37482	ESTs Highly similar to COATOMER ZETA SUBUNIT [Bos taurus]
23863	1	T93870	Hs.17265	ESTs
23946	1	T93078	Hs.17717	EST
15143	1	U79257	Hs.86021	Human clone 23932 mRNA sequence
9711	1	L44334	Hs.10432	ESTs Weakly similar to BENOMYL/ETHOTREXATE RESISTANCE PROTEIN [Candida albicans]
22544	1	R74235	Hs.80844	EST - RC_R52088 Homo sapiens mRNA for KIAA0573 protein partial cds
41506	1	R52088	Hs.80844	EST - RC_R52088
39345	1	C21105	Hs.7768	Homo sapiens FGF-1 intracellular binding protein (FIBP) mRNA complete cds
22272	1	R56922	Hs.26590	ESTs
16434	1	AA024464	Hs.61199	ESTs
17255	1	AA024464	Hs.61199	EST - RC_AA084412
22692	1	R85711	Hs.34183	ESTs
36830	1	AA605189	Hs.116415	ESTs
9179	1	D50312	Hs.102308	Human mRNA for uKATP-1 complete cds
42547	1	W73946	Hs.102308	EST - RC_W73946
36195	1	AA421144	Hs.10441	ESTs
29355	1	H70121	Hs.79592	ESTs
34608	1	AA281765	Hs.10441	ESTs
20779	1	N67553	Hs.16917	ESTs
11081	1	AA148626	Hs.34274	ESTs
12151	1	AA291269	Hs.24642	ESTs
39635	1	H52379	Hs.52379	EST - RC_H52379
7157	1	AA037199	Hs.9899	ESTs
17858	1	AA156586	Hs.72145	ESTs
34685	1	AA302831	Hs.57732	Homo sapiens p38beta2 MAP kinase mRNA complete cds
18445	1	AA232549	Hs.87068	ESTs
22524	1	R72597	Hs.87068	EST - RC_R72597
19224	1	H12448	Hs.124570	ESTs Weakly similar to unknown protein [H.sapiens]
18803	1	F06988	Hs.5294	ESTs
13810	1	AA464589	Hs.23294	ESTs Weakly similar to HSP90 [C.elegans]
18070	1	AA180352	Hs.72733	ESTs
17637	1	AA184750	Hs.72499	ESTs
36115	1	AA620736	Hs.112893	EST
22517	1	R71882	Hs.25966	ESTs Highly similar to 40S RIBOSOMAL PROTEIN S27A [Homo sapiens Cavia porcellus]

FIGURE 7 (CONT.)

16906	1	AA058555	Hs.63392	EST	
14251	1	AA487049	Hs.32501	ESTs	
23923	1	T96407	Hs.17812	ESTs	
21177	1	R06569	Hs.19721	ESTs	
25705	1	AA131921	Hs.71030	ESTs	
19605	1	H57725	Hs.124031	ESTs	
19668	1	H47556	Hs.33891	EST	
36593	1	AA432389	Hs.95702	ESTs	
14036	1	AA482107	Hs.5473	ESTs	
20959	1	N68825	Hs.16762	ESTs	
23849	1	T93113	EST - RC_T93113	ESTs	
16285	1	AA207122	Hs.86316	ESTs	
32275	1	AA358530	Hs.97363	ESTs	
10262	1	R77869	Hs.110493	ESTs	
21757	1	R40789	Hs.21299	ESTs	
21541	1	R31607	Hs.24420	ESTs	
16873	1	AA056258	Hs.63264	EST	
19646	1	H46006	Hs.31677	ESTs	
23719	1	T86160	Hs.138506	ESTs	
15608	1	H41581	Hs.31582	ESTs Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]	
17382	1	AA102731	Hs.109072	ESTs	
16564	1	AA055971	Hs.63238	ESTs	
10697	1	AA111881	Hs.9192	ESTs	
17028	1	AA070178	EST - RC_AA070178	ESTs	
15220	1	H12318	Hs.24324	ESTs	
9726	0	L44574	Hs.125235	ESTs	
24570	0	Z36891	Hs.27150	ESTs	
22167	0	R53021	Hs.25873	ESTs	
42537	0	W73417	Hs.103183	EST	
18806	0	F10005	Hs.12569	ESTs	
16585	0	AA033948	Hs.4236	ESTs	
17309	0	AA086232	Hs.68717	EST Moderately similar to maiterin transposase [H.sapiens]	
22813	0	R97419	Hs.35718	ESTs	
16429	0	AA022963	Hs.61772	EST	
22013	0	R48336	Hs.25377	EST	
8439	0	AA431277	Hs.32419	ESTs	
22034	0	T10046	Hs.4265	ESTs	
13663	0	AA423386	Hs.1191	Human mRNA for KIAA0073 gene partial cds	
10122	0	R31746	EST - R31745	EST	
10196	0	AA195263	Hs.56001	EST	

FIGURE 7 (CONT.)

33249	0	W7257	Hs.57836	ESTs
16806	0	AA063378	Hs.144270	ESTs
18063	0	AA229829	Hs.66902	EST
34154	0	AA219304	Hs.74561	ALPHA-2-MACROGLOBULIN PRECURSOR
16222	0	AA011210	Hs.95044	ESTs
17174	0	AA079306	EST - RC_AA079306	

Primary Key	fold upregulated at Tumor over normal	Accession	Ungene Descriptor	ORF structural info
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031208	H.sapiens mRNA for kinesin-2	other
25215	>10	AA035540	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
25282	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS.
10747	>10	AA055941	ESTs	other
10748	>10	AA055952	ESTs	other
16993	>10	AA065300	Human mRNA for KIAA0035 gene partial cds	other
17051	>10	AA070801	ESTs	TM
10940	>10	AA084104	ESTs	other
7296	>10	AA085661	ESTs	other
7325	>10	AA090642	ESTs Weekly similar to HYPOTHETICAL 36 7 KD PROTEIN C22F.02C IN CHROMOSOME 1 [Schizosaccharomyces pombe]	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17558	>10	AA128407	ESTs	other
25669	>10	AA128978	ESTs	?
17600	>10	AA130596	ESTs	other
10992	>10	AA132523	Homo sapiens BAC clone RG119C02 from 7p15	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA148530	TM
25806	>10	AA149007	EST	?
11121	>10	AA156359	Human TAR DNA-binding protein-43 mRNA complete cds	?
11180	>10	AA164289	ESTs	other
25925	>10	AA164484	ESTs Weekly similar to CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (H.sapiens)	other
25934	>10	AA165355	Human clone xta unknown protein mRNA complete cds	?
17987	>10	AA169379	ESTs	other
18008	>10	AA171895	Homo sapiens clone 24748 and 24750 mRNA sequences	TM
33953	>10	AA173290	Human HCCA1 mRNA long transcript and alternatively spliced forms complete cds	other
33980	>10	AA180223	CAMP-DEPENDENT PROTEIN KINASE TYPE B-ALPHA REGULATORY CHAIN	other
34013	>10	AA190086	EST - RC_AA190086	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
16290	>10	AA206801	ESTs	?
34105	>10	AA207123	ESTs	SS.
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA for apolipoprotein E receptor 2 complete cds	TM
18362	>10	AA223912	Ribonuclease L (2'-5'-oligoadenylate synthetase-dependent) inhibitor	other
18392	>10	AA227751	ESTs	SS.
34188	>10	AA228030	ESTs	TM
34197	>10	AA232915	Homo sapiens clone 23797 and 23917 mRNA partial cds	other
25948	>10	AA234365	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1) mRNA complete cds	?
25951	>10	AA234556	EST	?

FIGURE 8

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11561	>10	AJ236533	Eve-1	other
20059	>10	AJ236685	ESTs	other
26100	>10	AJ242835	Human mRNA for KIAA0391 gene complete cds	other
11603	>10	AJ243052	ESTs Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]	other
7785	>10	AJ243375	EST - AJ243375	other
34372	>10	AJ251973	ESTs	?
26240	>10	AJ252282	Human mRNA for KIAA0152 gene complete cds	TM
34382	>10	AJ252512	ESTs	other
34391	>10	AJ252703	EST - RC_AJ252703	other
26374	>10	AJ253011	ESTs	?
34400	>10	AJ253400	ESTs	other
20291	>10	AJ263422	ESTs	?
26355	>10	AJ266379	ESTs	other
11613	>10	AJ266156	ESTs	other
34510	>10	AJ278721	ESTs	?
26545	>10	AJ278979	ESTs	other
26574	>10	AJ279504	ESTs	other
34584	>10	AJ280018	DNA polymerase gamma	other
34561	>10	AJ280298	ESTs	TM
26628	>10	AJ280641	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L39 [Rattus norvegicus]	TM
11969	>10	AJ280670	ESTs	SS
34575	>10	AJ280738	ESTs	TM
26677	>10	AJ281636	ESTs	?
26700	>10	AJ282197	EST	?
34672	>10	AJ284372	ESTs	other
34692	>10	AJ285079	ESTs	other
12143	>10	AJ290991	ESTs	other
6092	>10	AJ316272	ESTs	TM
34804	>10	AJ321745	EST	other
8111	>10	AJ323767	ESTs	other
8125	>10	AJ330771	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
26916	>10	AJ331393	ESTs	other
26920	>10	AJ342402	ESTs	other
26935	>10	AJ347193	ESTs Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 [Caenorhabditis elegans]	TM
35038	>10	AJ350541	ESTs Moderately similar to URACIL-DNA GLYCOSYLASE 1 PRECURSOR [H.sapiens]	TM
35049	>10	AJ350687	ESTs	other
35106	>10	AJ371561	EST Weakly similar to putative p150 [H.sapiens]	?
35197	>10	AJ388120	ESTs	other
35277	>10	AJ388536	ESTs	other
35309	>10	AJ388660	EST	other
35322	>10	AJ396710	H sapiens RNA for CLCN3	TM
27037	>10	AJ400198	ESTs	TM
35495	>10	AJ400527	ESTs	?
27046	>10	AJ400670	Human sapiens mRNA for KIAA0582 protein partial cds	other
35500	>10	AJ400715	ESTs	other
12480	>10	AJ403116	Human sapiens U-arrFNP-associated cyclophilin (USA-CYP) mRNA complete cds	other
35693	>10	AJ405485	ESTs Weakly similar to similar to t complex testis-specific protein [C. elegans]	other
35697	>10	AJ405517	ESTs	other
35766	>10	AJ406169	Human sapiens KIAA0431 mRNA partial cds	other
35769	>10	AJ406206	ESTs	other
35798	>10	AJ410231	ESTs	other

FIGURE 8 (cont.)

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35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35958	>10	AA412550	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly similar to H ¹ ALU SUBFAMILY J WARNING ENTRY III [H. sapiens]	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424603	EST	?
36371	>10	AA426017	ESTs	TM
36385	>10	AA426553	ESTs	other
36405	>10	AA426406	Homo sapiens mRNA for KIAA0530 protein partial cds	other
36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA430726	SS
36685	>10	AA433910	ESTs	other
36728	>10	AA435610	EST - RC_AA435610	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS, TM
13143	>10	AA436619	ESTs	SS
36858	>10	AA442060	ESTs	other
36862	>10	AA442082	ESTs	?
36881	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly similar to H ¹ ALU SUBFAMILY J WARNING ENTRY III [H. sapiens]	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly similar to H ¹ ALU CLASS C WARNING ENTRY III [H. sapiens]	other
37074	>10	AA446344	ESTs	SS
37084	>10	AA446485	Homo sapiens Ran binding protein 2 (RanBP2alpha) mRNA partial cds	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA447714	other
37168	>10	AA447772	ESTs	?
37246	>10	AA449311	Homo sapiens mitotic checkpoint protein kinase (BUB1) mRNA complete cds	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454610	ESTs	?
37458	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA455248	other
37548	>10	AA456641	ESTs	TM
37601	>10	AA456864	ESTs	other
37611	>10	AA456996	Human signalling lymphocytic activation molecule (SLAMF) mRNA complete cds	SS, TM
37615	>10	AA459101	Human serine/threonine kinase mRNA partial cds	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens orphan G protein-coupled receptor H338 mRNA complete cds	other
37777	>10	AA464860	Homo sapiens Jnk2 kinase mRNA complete cds	other
8648	>10	AA465016	Homo sapiens serine protease-like protease (wsc1) mRNA complete cds	?
37816	>10	AA469954	EST	?
37829	>10	AA470084	ESTs	other
28015	>10	AA472421	ESTs	other
37978	>10	AA478294	EST - RC_AA478294	other
37979	>10	AA479295	ESTs highly similar to RING CANAL PROTEIN [Drosophila melanogaster]	other

FIGURE 8 (cont.)

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37983	>10	AA479348	H sapiens mRNA for SYT	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA485724	other
28122	>10	AA485928	ESTs Weakly similar to LOK [H. musculus]	other
38167	>10	AA487207	EST - RC_AA487207	other
38172	>10	AA487424	EST - RC_AA487424	other
38179	>10	AA487492	Homo sapiens clone 23592 mRNA sequence	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA489791	other
38316	>10	AA490500	Homo sapiens ribonuclease P protein subunit p20 (RPP20) mRNA complete cds	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS.
38460	>10	AA504462	ESTs	other
38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA for transcriptional activator hSNF2b complete cds	other
38601	>10	AA598738	ESTs	?
38623	>10	AA599639	ESTs	other
38628	>10	AA609177	ESTs	TM
38638	>10	AA609215	EST - RC_AA609215	?
38667	>10	AA609318	Human cdt-b mRNA complete cds	TM
38671	>10	AA609333	EST	?
38670	>10	AA609749	ESTs	other
38684	>10	AA620839	ESTs Moderately similar to H11 ALU SUBFAMILY J WARNING ENTRY H11 [H. sapiens]	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA620552_y	?
39110	>10	AA620709	ESTs Weakly similar to HYPOTHETICAL 90.8 KD PROTEIN TOSHIO 7 IN CHROMOSOME 8 [C. elegans]	other
39178	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens protein phosphatase with EF-hand-1 (PPEF-1) mRNA complete cds	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H sapiens histone H4 gene	?
8963	>10	AFFX: HUMTFRRM115 07	AFFX:HUMTFRRM11507_M	?
33890	>10	AFFX: HUMTFRRM115 07	AFFX:HUMTFRRM11507_5	?
39302	>10	C14944	ESTs	other
39329	>10	C20787	EST	?
28644	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYROSINE PHOSPHATASE 2C	other
226	>10	D13645	Human mRNA for KIAA0020 gene complete cds	other
9127	>10	D30037	PHOSPHATIDYLINOSITOL	other
459	>10	D38293	Human mRNA for clathrin-like protein complete cds	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymidine kinase 2 (TK2) mRNA complete cds	other
39436	>10	D52662	Human Ca ²⁺ -dependent activator protein for secretion mRNA complete cds	TM
14708	>10	D59388	EST	?

FIGURE 8 (cont.)

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39488	>10	D60831	ESTs	other
39504	>10	D60632	ESTs	other
765	>10	D86095	Prostaglandin E receptor 3 (subtype EP3) (ratimmune products)	?
787	>10	D86968	Human mRNA for KIAA0215 gene complete cds	other
789	>10	D86971	Human mRNA for KIAA0217 gene partial cds	other
39529	>10	F02202	ESTs	?
38535	>10	F02450	ESTs Moderately similar to unknown protein [H.sapiens]	TM
18676	>10	F04022	ESTs	other
18718	>10	F04815	ESTs	other
18762	>10	F09456	ESTs	other
18762	>10	F09738	ESTs	other
29060	>10	F13655	ESTs Moderately similar to III ALU SUBFAMILY SB1 WARNING ENTRY III [H.sapiens]	other
19001	>10	H02890	ESTs	other
19164	>10	H10895	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17606	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19588	>10	H20165	EST	?
39632	>10	H26278	EST - RC_H26279	other
19591	>10	H40668	ESTs	other
28229	>10	H46459	Human mRNA for KIAA0196 gene complete cds	other
19727	>10	H52702	ESTs	?
19787	>10	H56679	ESTs	other
39995	>10	H82474	EST	SS, TM
29331	>10	H85116	ESTs	TM
29344	>10	H86839	EST	?
42064	>10	H72283	Human mRNA for KIAA0255 gene partial cds	other
42083	>10	H73466	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3	other
19948	>10	H78263	ESTs	TM
42204	>10	H88296	EST - RC_H88296	other
29523	>10	H85353	ESTs Weakly similar to line-1 protein ORF2 [H.sapiens]	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HQ2036-HT2090	EST - HQ2036-HT2090	?
1156	>10	HQ3344-HT3521	EST - HQ3344-HT3521	?
1210	>10	HQ37-HT37	EST - HQ37-HT37	?
1346	>10	HQ4716-HT5155	EST - HQ4716-HT5155	?
1349	>10	HQ4747-HT5195	EST - HQ4747-HT5195	?
1445	>10	J03027	MHC class I protein HLA-G	?
1570	>10	K01383	EST - K01383	?
1864	>10	L07541	Replication factor C (activator 1) 3 (38kD)	other
1852	>10	L17326	Human FEZ2 mRNA partial cds	TM
1856	>10	L18920	MELANOMA-ASSOCIATED ANTIGEN 2	?
1863	>10	L19161	TRANSLATION INITIATION FACTOR 2 GAMMA SUBUNIT	other
2070	>10	L37378	Homo sapiens guanylyl cyclase (RelGC-2) mRNA complete cds	SS, TM
2123	>10	L40396	Homo sapiens (clone z2271) mRNA fragment	other
2144	>10	L41349	Phospholipase C beta 4	SS,
9723	>10	L44542	ESTs	other
2168	>10	L47276	EST - L47276	other

FIGURE 8 (cont.)

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2343	>10	M13353	Eukaryotic translation initiation factor 4E	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransferase 4 [alpha (13) fucosyltransferase myeloid-specific]	TM
3021	>10	M68041	Protein tyrosine phosphatase non-receptor type 4	other
3163	>10	M84424	Cathepsin E	?
3196	>10	M86917	Oxysterol binding protein	other
20008	>10	N20054	ESTs Weakly similar to putative p150 [H.sapiens]	?
29795	>10	N20641	ESTs Highly similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 [Homo sapiens]	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly similar to TUBULIN GAMMA CHAIN [Euplates octocarinatus]	other
29992	>10	N23003	ESTs	TM
40498	>10	N25095	Homo sapiens citrate synthase mRNA complete cds	SS
40599	>10	N33024	ESTs	SS
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mRNA for diubiquitin	other
23304	>10	N34686	Homo sapiens clone 23515 mRNA sequence	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40594	>10	N35366	ESTs	other
40604	>10	N39893	Homo sapiens KIA0428 mRNA complete cds	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FACTOR RBP140	other
30610	>10	N50138	EST	?
30617	>10	N50645	ESTs	other
30631	>10	N50807	EST	?
30790	>10	N52035	EST	?
20564	>10	N58443	ESTs	TM
40760	>10	N57927	ESTs Weakly similar to ELL [M.musculus]	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS
20657	>10	N62869	ESTs	other
31136	>10	N63512	ESTs Weakly similar to MD1F1.4 [C.elegans]	TM
40627	>10	N64051	Homo sapiens Werner syndrome gene complete cds	other
31310	>10	N66831	EST	?
40676	>10	N67607	Human Rho-associated coiled-coil containing protein kinase p16ORCK mRNA complete cds	other
20791	>10	N68057	Homo sapiens telomeric repeat binding factor (TRF 1) mRNA complete cds	?
40905	>10	N68736	ESTs	other
40911	>10	N69114	H.sapiens mRNA for orphan nuclear hormone receptor	other
40913	>10	N69218	ESTs	other
31484	>10	N69466	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31816	>10	N80774	Homo sapiens mRNA for KIA0292 gene partial cds	other
31972	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93618	ESTs	other
32034	>10	N96925	ESTs Moderately similar to DMR-N9 PROTEIN [H.sapiens]	other
41107	>10	RD1634	ESTs	other
41163	>10	RD8176	ESTs	other
21236	>10	RD8564	Plasminogen-like protein	other

FIGURE 8 (cont.)

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21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27675	EST - RC_R27675	other
41381	>10	R42276	H sapiens mRNA for TRE5	?
32189	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly similar to ORF YOR258w (S. cerevisiae)	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
32258	>10	R55523	ESTs	other
22258	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA for rod photoreceptor protein complete cds	other
22372	>10	R62631	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly similar to PHENYLALANINE tRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC (Saccharomyces cerevisiae)	other
41654	>10	R76457	THROMBOXANE-A SYNTHASE	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R83260	EST - RC_R83260	other
22793	>10	R96208	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66595	SQUAMOUS CELL CARCINOMA ANTIGEN 1	other
3522	>10	S80267	Spleen tyrosine kinase	other
41793	>10	T03887	ESTs	?
23186	>10	T40530	ESTs Weakly similar to B0035.14 [C elegans]	other
23560	>10	T58531	ESTs	other
23635	>10	T61116	ESTs	other
41777	>10	T79786	ESTs	?
23623	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Homo sapiens E2F-related transcription factor (DP-1) mRNA complete cds	other
23759	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92960	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like peptide-1 receptor	SS, TM
3659	>10	U04313	Protease inhibitor 5 (masepin)	?
3799	>10	U10690	Human MAGE-5a antigen (MAGE5a) gene complete cds	?
3870	>10	U14518	Centromere protein A (17kD)	other
3913	>10	U16261	Human MDA-7 (mda-7) mRNA complete cds	SS,
4029	>10	U21090	Human DNA polymerase delta small subunit mRNA complete cds	other
4157	>10	U28811	Human cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA complete cds	other
4178	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15006	>10	U30246	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM

FIGURE 8 (cont.)

4193	>10	U31116	Human beta-sarcoglycan A3b mRNA complete cds	TM
4306	>10	U36708	Homo sapiens platelet cGMP-DE mRNA complete cds	TM
4362	>10	U39817	Blooms syndrome	other
4306	>10	U40622	DNA repair protein XRCC4	other
4306	>10	U40714	Human lysoyl-HRNA synthetase mRNA complete cds	other
4455	>10	U43944	MALATE OXIDOREDUCTASE	other
4477	>10	U45880	Human MAP-like protein ILP mRNA complete cds	other
4600	>10	U55766	Human Rev interacting protein Rip-1 mRNA complete cds	TM
4702	>10	U57341	EST - U57341	other
4713	>10	U57721	Human L-tyrosine hydrolase mRNA complete cds	other
4787	>10	U61145	Human enhancer of zeste homolog 2 (EZH2) mRNA complete cds	other
4862	>10	U55437	Human homododecin-containing protein (H4NF) mRNA complete cds	?
4945	>10	U69108	Homo sapiens mRNA for TRAF5 complete cds	other
4975	>10	U71068	Human MEK5 mRNA complete cds	other
4994	>10	U72514	Human C2f mRNA complete cds	other
5002	>10	U72761	Human karyopherin beta 3 mRNA complete cds	other
5021	>10	U73524	Human putative ATP/GTP-binding protein (HEAB) mRNA complete cds	TM
5148	>10	U79716	Human reelin (RELN) mRNA complete cds	SS
5214	>10	U83303	H sapiens mRNA for granulocyte chemotactic protein	?
5243	>10	U85946	Human brain secretory protein hSec10p (HSEC10) mRNA complete cds	other
32789	>10	V02779	ESTs Moderately similar to kinesin-73 [D.melanogaster]	other
42354	>10	W15346	ESTs	other
42390	>10	W40150	Homo sapiens chromosome-associated polypeptide (HCAP) mRNA complete cds	other
33006	>10	W46286	ESTs Weakly similar to ZK1058.5 [C.elegans]	TM
33020	>10	W46891	ESTs Weakly similar to polypeptide N-acetylglucosaminyltransferase [H.sapiens]	other
33108	>10	W59961	Human mRNA for KIAA0385 gene complete cds	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79634	ESTs Weakly similar to thotekin [M.musculus]	other
33377	>10	W81219	ESTs Weakly similar to F4686.7 [C.elegans]	other
42602	>10	W86423	ESTs	TM
33558	>10	W90705	Murine leukemia viral (bmi-1) oncogene homolog	other
33616	>10	W93726	Protease inhibitor 5 (maspin)	other
33666	>10	W95876	ESTs	TM
5510	>10	X05360	Cell division cycle 2 G1 to S and G2 to M	?
5558	>10	X07876	Wingless-type MMTV integrin site 2 human homolog	SS
5603	>10	X14253	Taratacanceroma-derived growth factor 1	TM
5619	>10	X14850	HISTONE H2AX	SS
5623	>10	X14975	T-CELL SURFACE GLYCOPROTEIN CD1E PRECURSOR	?
5692	>10	X17644	G1 to S phase transition 1	other
5780	>10	X54925	Matrix metalloproteinase 1 (interstitial collagenase)	other
5799	>10	X55030	Asparitylglucosaminidase	SS
5802	>10	X55544	CYCLOC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-1	?
5857	>10	X58377	Human mRNA for adipogenesis inhibitory factor	other
5960	>10	X63375	ATPase Ca++ transporting plasma membrane 2 (HOTE redefinition of symbol)	TM
5963	>10	X63629	Cadherin 3 (P-cadherin)	SS, TM
5986	>10	X64810	Proprotein convertase subtilisin/kexin type 1	?
6041	>10	X67155	MITOTIC KINESIN-LIKE PROTEIN-1	other
6095	>10	X69062	Fragile X mental retardation 1	other

FIGURE 8 (cont.)

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6106	>10	X70583	SRV (sex determining region Y)-box 4	TM
6155	>10	X74331	DNA primase polypeptide 2A (58AD)	other
6167	>10	X74967	Ribonuclease L (2'5'-oligoadenylate synthetase-dependent) inhibitor	other
6188	>10	X76029	NEUROMEDIN U-25 PRECURSOR	TM
6215	>10	X81899	H.sapiens mRNA for p007.1 protein	other
6382	>10	X85133	H.sapiens RBO-1 mRNA	other
6384	>10	X85137	Human kinesin-like spindle protein HKSP (HGPS)	other
6438	>10	X80390	mRNA complete cds	?
6449	>10	X89996	UPACILON GLYCOXYLASE 1 PRECURSOR	?
6478	>10	X31646	H.sapiens mRNA for NIK apoptotic inducer protein	TM
6479	>10	X91653	H.sapiens mRNA for pur alpha extended 3'untranslated region	SS, TM
6494	>10	X92589	EST - X91653	?
6713	>10	X08564	H.sapiens mRNA for UDP-GalNAc polypeptide N-acetylglucosaminyl transferase	TM
6790	>10	Y12394	EST - Y08564	?
24915	>10	YEL003w	Homo sapiens angiotensin-converting enzyme (ACE) mRNA complete cds	other
42773	>10	YEL019wMM521	EST - YEL003w	?
24545	>10	Z38462	EST - YEL019wMM521	?
33713	>10	Z39427	ESTs	other
33791	>10	Z40863	ESTs	other
42766	>10	Z99394	ESTs Moderately similar to IRI ALU SUBFAMILY 5P	other
21564	>10	R33112	WARNING ENTRY III (H.sapiens)	other
26718	>10	AA282576	Human AF-4 mRNA complete cds	other
40113	9.9550509946	H78003	ESTs	?
10601	9.8979448276	AA059285	ESTs	?
37491	9.9513600842	AA455739	ESTs	?
23600	9.9272347683	T95789	ESTs	?
254	9.9198395324	D14857	ESTs	?
6685	9.8970827914	Z29331	Human mRNA for KIAA0101 gene complete cds	other
28693	9.8650766398	H97819	Ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)	other
26482	9.8705189024	AA262491	ESTs	SS,
23123	9.8695502035	T25306	ESTs	?
26525	9.8100399123	AA278392	ESTs	other
13110	9.7843356605	AA435840	ESTs	?
34863	9.7061597026	AA299794	Human sapiens mRNA for high mobility group protein HMO2a	other
35432	9.7034550063	D51691	EST	?
31312	9.6513325308	N68845	Phosphoenolpyruvate carboxyltransferase phosphoenolpyruvate synthetase	?
21112	9.6356446349	R01179	phosphoenolpyruvate carboxyltransferase	?
31572	9.6258420095	N71294	ESTs	?
17903	9.6221229759	AA160259	ESTs	?
20747	9.6094813734	N06942	ESTs	other
4676	9.5892229008	U55206	Human sapiens human gamma-glutamyl hydrolase (GGH)	TM
34363	9.5627061023	AA251567	mRNA complete cds	?
39094	9.540769898	AA520636	Human sapiens mRNA for KIAA0530 protein partial cds	other
3888	9.5372000133	U15128	ESTs	?
39366	9.506250529	D12184	Human beta-1,4-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
7674	9.4456059039	AA203742	ESTs	TM
4192	9.4329744134	U31099	ESTs	other
4507	9.422574945	U47050	Human DP1 prostanoil receptor (PTGDR) mRNA partial cds	TM
			Human putative calcium influx channel (htrp3) mRNA complete cds	TM

FIGURE 8 (cont.)

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35006	9 412026255	AA402227	ESTs Moderately similar to H-tropomodulin [H.norvegicus]	other
4970	9 3649551013	U70862	Human nuclear factor I-B2 (NF1B2) mRNA complete cds	?
19829	9 5432151573	H58813	EST	?
14837	9 2875894141	T40145	ESTs	TM
17336	9 2822148675	AA099585	ESTs	other
40541	9 2533263505	N30160	ESTs	other
29496	9 2487643833	H5434	EST	?
29943	9 1797074262	H24786	ESTs Moderately similar to Ht ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	TM
17997	9 1629681314	AA169033	EST	other
21320	9 1243453318	R11673	ESTs	other
13883	9 1178796537	AA476917	ESTs Weakly similar to No definition line found [C.elegans]	other
30539	9 0866887776	N49072	ESTs	other
32778	9 06777919549	W02053	EST	?
26380	9 0605593378	AA257012	EST	?
15808	9 0595933607	X95632	Human Abi interactor 2 (Abi-2) mRNA complete cds	other
40812	9 0012674244	H53418	ESTs	other
903	8 9640387968	D90070	ATL-derived PMA-responsive (APR) peptide	other
22674	8 9515777733	R87160	ESTs	TM
40607	8 93510132881	N52095	TRANSCRIPTION INITIATION FACTOR IF BETA SUBUNIT	other
15244	8 9195644974	W09904	ESTs	TM
32296	8 9058776567	R67075	Zinc finger protein X-linked	other
16269	8 8579636769	AA209487	ESTs	other
19682	8 8507628284	H47391	ESTs	other
41607	8 8339255117	R67668	CLEAVAGE SIGNAL-1 PROTEIN	other
2548	8 8280664599	M25807	Platelet factor 4	TM
7736	8 8279341243	AA232121	Human tyrosyl-tRNA synthetase mRNA complete cds	other
34490	8 7844537272	AA382354	ESTs	other
30658	8 7688013482	AA599477	ESTs	other
7528	8 765157554	AA149543	ESTs	other
39939	8 7585031142	H53454	EST - RC_H53454	other
25111	8 7232692309	AA020767	ESTs	other
21656	8 716167279	R38239	EST	?
30663	8 665982852	H04756	ESTs Highly similar to NADH:UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT [Bos taurus]	other
1042	8 652112224	HG2510-HT2606	EST - HG2510-HT2606	?
32330	8 6361115426	R77778	ESTs	other
25362	8 6239456487	AA059007	ESTs	other
27074	8 5900813076	AA401475	ESTs Weakly similar to C56B1.3 [C.elegans]	SS
3955	8 5298609183	U18259	MHC class II transactivator	other
4959	8 52646827	U70322	Human transportin (TRN) mRNA complete cds	?
2315	8 5259185008	M14123	EST - M14123_x01	?
37253	8 4936914632	AA449357	ESTs	other
39624	8 471316077	F10836	ESTs	?
23213	8 4589920887	T40891	ESTs	?
2798	8 455596435	M54995	Connective tissue activation peptide III	TM
41154	8 4413300141	R07499	ESTs	?
32479	8 4053686549	T16282	WEE1-LIKE PROTEIN KINASE	other
41261	8 358756515	R28279	Human clone 23548 mRNA sequence	other
19081	8 3583603183	H06701	ESTs Weakly similar to RHOMBOTIN-1 [H.sapiens]	other
21088	8 3105927559	R00545	ESTs	other
14723	8 3061679053	D59894	ESTs	other
37154	8 2994822341	AA447666	Human CENP-F kinetochore protein mRNA complete cds	other

FIGURE 8 (cont.)

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8068	8.283559635	AA313387	ESTs Highly similar to HYPOTHETICAL 84 7 KD PROTEIN ZK1098.1 IN CHROMOSOME II (C.elegans) elegans	other
7485	8.2816719348	AA1129547	ESTs	other
16501	8.2517569834	AA026969	ESTs	other
34527	8.2419153754	AA279091	ESTs	other
6700	8.1948675662	Y07867	H sapiens mRNA for Piro isolate 1	other
2832	8.1928816537	M58460	Human 75-kD autoantigen (PM-Scl) mRNA complete cds	other
11188	8.1862492468	AA172372	ESTs	TM
42293	8.183311054	T95333	ESTs Weakly similar to coded for by C. elegans cDNA yk110g1.3 (C. elegans)	TM
5443	8.1763317544	X02530	Interferon (gamma)-induced cell line protein 10.8kDa	SS
40537	8.1534810594	N70607	ESTs	TM
23371	8.1499436068	T59505	EST - RC_T59505	?
26272	8.133974519	AA252981	ESTs Weakly similar to KOTC11.10 gene product (C. elegans)	other
17306	8.1332403762	AA060201	ESTs	other
16497	8.1192326373	AA233795	ESTs	other
225	8.0944363901	D13644	Human mRNA for KIAA0019 gene complete cds	other
24525	8.0680187097	Z36347	ESTs	TM
7629	8.0700209554	AA248884	EST - AA248884	TM
32142	8.0739256775	R38715	Homo sapiens clone 24540 mRNA sequence	other
39067	8.0557766603	AA620405	ESTs	other
6235	8.0448957236	X76416	Casein alpha S1	TM
29517	8.0017586725	H88261	ESTs	other
28570	7.9852455973	C21104	Homo sapiens STAT-induced STAT inhibitor-2 mRNA complete cds	other
38944	7.9162087762	C21034	ESTs Moderately similar to valsalin factor eIF-2B gamma subunit (R. norvegicus)	other
18851	7.9002189759	H00580	ESTs	other
18853	7.8709160227	H00615	ESTs	other
18378	7.8564020916	AA226925	ESTs	other
19030	7.847878447	H58911	ESTs	other
36023	7.840035828	AA416981	ESTs	other
13347	7.83444414518	AA449238	ESTs	other
36814	7.8284591351	AA431466	ESTs	other
2192	7.8254072032	L48211	Homo Sapiens angiotensin II receptor gene complete cds	?
33016	7.8006574068	VH6577	H sapiens mRNA for ESM-1 protein	other
17215	7.7941954038	AA083044	ESTs	other
34894	7.7659738105	AA311801	EST	?
40614	7.895001222	N39257	ESTs	other
36295	7.6834740899	AA424534	ESTs	other
19564	7.6744322788	H38833	ESTs	TM
16914	7.6686406336	AA059065	ESTs	SS
39067	7.6378078107	AA412694	Human splicing factor SRp55-2 (SRp55) mRNA complete cds	other
21072	7.6364823402	R38635	ESTs	other
19918	7.6303275631	H69787	ESTs	?
10511	7.6297744492	AA054482	ESTs Highly similar to KERATIN TYPE I CYTOSKELETAL 14 (Homo sapiens)	other
17721	7.6057911016	AA136590	ESTs	?
42302	7.6031859697	T96130	EST	SS
26134	7.6000610363	AA243763	ESTs	other
18766	7.5621798008	F09497	ESTs	other
34482	7.501590404	AA262430	ATL-derived PSA-responsive (APR) peptide	other
270	7.4512152125	D14822	EST - D14822	other
39875	7.4177746886	AA412738	ESTs	other
28842	7.4095808671	N21688	ESTs	?

FIGURE 8 (cont.)

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35869	7 3913043319	AA388555	ESTs	other
19979	7 3869157166	H88477	ESTs	other
5793	7 3855664925	X54942	CDC28 protein kinase 2	other
19578	7 380969715	H87770	EST - RC_H87770	other
1280	7 3691089318	HG4126-HT4396	EST - HG4126-HT4396	?
31571	7 3676263454	H71250	ESTs	other
23765	7 3541191734	T90443	ESTs Weakly similar to KIAA0376 [h.sapiens]	?
35123	7 3397933455	AA380927	EST	?
38292	7 3341118467	AA489247	ESTs	other
38216	7 3282021037	AA488861	ESTs	other
29418	7 2489407005	H77915	EST - RC_H77915	?
4834	7 1980651054	U63541	Human mRNA expressed in HCNICC livers and MuT-4 proliferating cells partial sequence	other
42604	7 1913036522	V65903	ESTs	other
6111	7 156000198	X71125	H.sapiens mRNA for glutamine cytosyltransferase	TM
41773	7 1544749616	T03024	ESTs Weakly similar to ribosomal protein L7 [H.sapiens]	other
9951	7 1363526365	H71513	ESTs	other
28109	7 0941968224	AA465212	ESTs	other
988	7 0783044659	HG2160-HT2230	EST - HG2160-HT2230	?
20848	7 0610666511	N22107	ESTs	other
30628	7 0607950168	N50744	ESTs	other
22567	7 0225726353	R77771	ESTs	TM
9347	7 006323071	H03689	ESTs	TM
11696	7 0026773299	AA252894	ESTs	other
40964	7 001009633	N24870	EST	?
193	6 9767029188	D10923	PROBABLE G PROTEIN-COUPLED RECEPTOR HM74	TM
18305	6 9740536051	AA214346	Collagen type IV alpha 4	other
6076	6 9699682357	X89141	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	other
26741	6 902658703	AA283198	ESTs	other
35069	6 8892865465	AA358397	EST	?
23504	6 8597132583	T71042	ESTs	other
299	6 8624513029	D16815	Human sapiens orphan nuclear hormone receptor BD73	other
40583	6 8609902023	H34655	mRNA 3' and ESTs	other
31428	6 8623762224	H65594	ESTs	other
8169	6 8606959737	X75091	SET PROTEIN	other
39524	6 8567255171	F01905	MALATE OXIDOREDUCTASE	other
34578	6 8430089430	AA280037	ESTs	other
38679	6 837527995	AA599920	Small inducible cytokine A5 (RANTES)	other
23936	6 8251471504	T96330	ESTs	other
0226	6 8161321394	D65377	Man (Drosophila) homeo box homolog 2	other
19188	6 8067351968	H11255	ESTs Highly similar to ACTIN LIKE PROTEIN [Bos taurus]	TM
18185	6 7882146811	AA194963	Human sapiens mRNA for osteoclastogenesis inhibitory factor (OCIF) complete cds	other
27028	6 757529124	AA399630	ESTs Weakly similar to KIAA0371 [H.sapiens]	other
41280	6 7519531681	R37265	EST	other
34511	6 7364448730	AA278298	EST - RC_AA278298	other
1566	6 7056020716	J06514	EST - J06514	?
25675	6 6892297448	AA129757	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
5614	6 6564342828	X96088	CYTOCHROME P450 VII	SS
13651	6 6236291607	AA470145	ESTs	other
29794	6 6026313352	N20598	ESTs	other
39333	6 5902832643	C20910	Cydan B1	other
3770	6 5835303599	U06609	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (NFkB105)	other

FIGURE 8 (cont.)

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31831	6.5829933764	N89894	ESTs	?
33063	6.5806125026	W53000	Homo sapiens clone 24431 mRNA sequence	other
20326	6.5640064836	N35583	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	?
34384	6.5535703492	AA325237	ESTs	other
25599	6.5490481931	AA114091	Human (cdna 851) B1-cadherin mRNA complete cds	other
39749	6.5369363254	H14988	ESTs	other
42396	6.5200567072	W85900	ESTs	?
39606	6.5119482185	F10243	ESTs Weakly similar to h1 ALU CLASS B WARNING ENTRY III [H.sapiens]	?
14617	6.5105504748	C14983	ESTs	other
27831	6.46670014	AA456944	ESTs	?
34996	6.4466517783	AA312551	EST	?
27360	6.4434306906	AA425350	ESTs	other
20126	6.4326610424	N22015	ESTs	TM
6663	6.4324809977	Y00291	RETINOIC ACID RECEPTOR BETA-2	TM
30692	6.4196630207	N51563	ESTs	other
36472	6.4189542265	AA428633	EST	?
9578	6.3961768753	H87652	Homo sapiens bicucullin (BICD) mRNA complete cds	other
39070	6.3818496159	H05266	ESTs	other
22697	6.3652792447	R89218	ESTs	other
37308	6.3647804993	AA451694	EST	TM
16101	6.3517262902	AA002147	EST	?
20629	6.3406654401	N58788	ESTs	other
36100	6.3364146287	AA417740	ESTs	?
15488	6.3282590241	V08097	Homo sapiens clone 23711 unknown mRNA partial cds	other
38667	6.3131273544	AA432136	ESTs	other
30766	6.3115037824	N52627	EST - RC_N52627	?
32882	6.2745311453	W37683	ESTs	TM
18072	6.2675797205	AA180448	EST	?
18231	6.2652604063	AA189747	Human mRNA for KIAA0096 gene partial cds	other
36262	6.2514168678	AA489814	EST	?
28125	6.250317021	AA486073	ESTs	other
37464	6.2484456382	AA451747	ESTs	?
36618	6.1948282223	AA431478	ESTs	other
5082	6.1831116615	U76524	Human G1 binding protein mRNA partial cds	other
1441	6.1772870339	J02963	Intrigins alpha 2b (platelet) glycoprotein IIB of fibrin complex antigen CD41B	other
42105	6.14875944	T67710	ESTs	?
6061	6.1354663141	X06314	Glutathione peroxidase 2 gastrointestinal	SS,
32570	6.1156028796	T30222	ESTs Weakly similar to tetrazocine transporter-like protein [M.musculus]	TM
32504	6.1019612076	T17063	EST	?
23336	6.0977927604	T56804	EST	?
10867	6.0970991075	AA088458	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
30883	6.0911993489	H56923	EST	?
14528	6.0858006433	AA820285	ESTs	TM
29454	6.0685955036	H81306	EST	?
6798	6.0539173278	Y13153	Homo sapiens mRNA for tyrosine 3-monooxygenase	TM
21248	6.0525426545	R06871	ESTs	?
21940	6.0499964138	R44538	ESTs	?
29056	6.045247653	F10927	Homo sapiens clone 23636 mRNA sequences	other
18774	6.0446826953	F09609	ESTs	?
36722	6.0172343991	AA435512	ESTs	SS,
18092	6.0034342969	AA179845	ESTs Moderately similar to rabies virus-6 [M.musculus]	other

FIGURE 8 (cont.)

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22969	5.9992817406	T16305	ESTs	other
41745	5.9606423898	R95885	ESTs	?
4787	5.9594877658	AA504307	X-LINKED HELICASE II	other
20550	5.9840617795	N55613	ESTs	other
26470	5.9417764101	AA262179	ESTs	other
16574	5.9366497569	AA031926	EST	other
893	5.9168533785	D80007	Human mRNA for KIAA0185 gene partial cds	other
4093	5.914630973	U25182	Human endonuclease AOE37-2 mRNA complete cds	TM
1192	5.908626407	HG3546-HT3744	EST - HG3546-HT3744	?
22966	5.8964735623	T10240	ESTs	other
36723	5.891606429	AA435524	EST	?
2114	5.8844985506	LA2084	EST - LA2084	other
26872	5.868238789	AA291137	ESTs	other
6602	5.8663883018	X96266	EST - X96266_cds2	other
42701	5.8594403433	Z38612	ESTs	other
28573	5.84591116	C21110	ESTs	other
18290	5.8189427595	AA211901	ESTs	other
732	5.8043917941	D83761	Human mRNA for KIAA0197 gene partial cds	other
5330	5.8014145611	U91327	EST - U91327	?
33503	5.7990715189	W88720	EST	?
2583	5.7797505864	M26167	Human platelet factor 4 variation 1 (PF4v1) gene complete cds	?
34705	5.7658062154	AA286907	ESTs: Weakly similar to putative p150 [H sapiens]	other
42065	5.7594391043	W83659	ESTs	other
36160	5.7539310793	AA487495	EST - RC_AA487495	other
4244	5.7476730309	U33285	Human chromosome segregation gene homolog CAS mRNA complete cds	TM
32822	5.7416957453	W15834	ESTs	TM
3977	5.7245885557	U18991	Retinal pigment epithelium-specific protein (SBD)	?
24573	5.7202366165	Z39301	ESTs	TM
6928	5.7120261126	Z46629	SRY (sex-determining region Y)-box 9 (campomelic dysplasia autosomal sex-reversal)	?
38726	5.7030796258	AA688733	ESTs	other
39290	5.6892372056	C14573	Human mRNA for KIAA0029 gene partial cds	other
11405	5.6818873790	AA322231	ESTs	other
22538	5.6792005591	R73567	Homo sapiens meltrin-L precursor (ADAM12) mRNA complete cds	TM
40747	5.6605383208	N56872	Homo sapiens clone 22 mRNA alternative splice variant alpha-1 complete cds	TM
31596	5.6554024604	N72094	ESTs	other
6329	5.6419652818	X82279	EST - X82279	?
31578	5.6273323661	N71361	ESTs	other
33207	5.6271518462	W70051	H.sapiens mRNA for M-phase phosphoprotein mpp9	other
2545	5.6105860146	M25783	Cyclin B1	other
22580	5.5988402647	R79156	ESTs	other
33592	5.5935314518	W93127	ESTs	other
28843	5.5734698755	D00252	ESTs	other
6180	5.5689030619	X74794	CDC21 HOMOLOG	other
37987	5.561340667	AA478666	ESTs	other
42515	5.5217686611	W72116	Homo sapiens clone Z3622 mRNA sequence	other
4732	5.5130066527	U58522	Human huntingtin interacting protein (HIP2) mRNA complete cds	other
3299	5.5099550678	M95523	Hydroxymethylbilane synthase	?
26320	5.4734069181	AA599574	ESTs	?
746	5.4712809599	D84454	Human mRNA for UDP-galactose translocator complete cds	TM
39373	5.4635804954	C21517	ESTs	other
3117	5.4398413537	MB1182	Peroxisomal membrane protein 1 (70kD Zellweger syndrome)	other

FIGURE 8 (cont.)

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21257	5.4343612441	R09195	ESTs Moderately similar to M-phase phosphoprotein 11 [H.sapiens]	other
31487	5.431864859	N69507	ESTs	other
28954	5.4137130511	P03153	ESTs	other
38928	5.389782721	AA609555	ESTs	other
29903	5.3722320622	N23366	EST	?
30925	5.347432815	N50295	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]	?
19091	5.3344615069	H07864	ESTs	TM
28209	5.3138551818	AA491250	ESTs	other
9470	5.3118897884	H46617	EST - H46617	other
9435	5.3070659656	H30201	EST - H30201	?
28552	5.2854432572	C20914	ESTs	other
27411	5.2540164267	AA426137	ESTs	other
30615	5.2524125264	N50556	ESTs	other
28313	5.2657977167	AA596309	ESTs	TM
39321	5.2649035364	C20632	ESTs	?
29934	5.2531047385	N24194	ESTs	other
1094	5.2496703122	HQ2646-HT2983	EST - HQ2646-HT2983	?
38578	5.2481126384	F06925	ESTs	TM
11232	5.2405794624	AA106504	ESTs Weakly similar to unknown [S.cerevisiae]	other
2466	5.2405493326	M21539	Human small proline rich protein (sprt) mRNA clone 1292	other
26643	5.2387756551	AA287450	ESTs	?
40331	5.2353385567	H97562	ESTs Weakly similar to SPERMATID-SPECIFIC PROTEIN T2 [Sepia officinalis]	other
8035	5.205796365	AA305116	EST - AA305116	other
28793	5.1955425722	N20593	ESTs Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]	other
34109	5.1481590107	AA210722	EST	?
26408	5.1425572257	AA258177	ESTs Weakly similar to ROSA26AS [M.musculus]	other
15263	5.1420729807	H15054	ESTs	TM
24586	5.1418069352	Z38810	ESTs	other
28589	5.1385559753	C21245	H.sapiens mRNA for apoptosis specific protein	other
5684	5.1121931412	X17098	Pregnancy-specific beta-1 glycoprotein 6	other
30710	5.1079347344	N51761	EST	?
35785	5.0973514948	AA408167	EST	?
26260	5.0863127861	AA258460	ESTs	?
2351	5.0648012092	M15796	Proliferating cell nuclear antigen	?
32262	5.0638877534	N5065	Homo sapiens clone 24739 mRNA sequence	other
41792	5.0737512465	T03886	ESTs	?
36710	5.0703898664	AA434411	ESTs	other
30909	5.0546865407	AA620628	ESTs	TM
42185	5.0539826381	T78951	ESTs	?
18745	5.0460321557	F09194	ESTs	other
35746	5.0396841996	AA406063	ESTs	?
35396	5.0354805581	AA399053	EST	?
36789	5.0312706878	AA435750	EST	?
36900	5.0279911548	AA436886	H.sapiens mRNA for M-phase phosphoprotein mpp8	other
27595	5.0244757201	AA443328	ESTs	TM
16290	5.0055611904	AA015145	ESTs	?
27117	5.0016148599	AA405098	ESTs Weakly similar to MOESIN/ZBRIN1/ADDON HOMOLOG (D.melanogaster)	other
4304	4.9951954387	U36764	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit	other
33458	4.9907402071	V86835	Homo sapiens mRNA for KIAA0636 protein complete cds	other
26693	4.9800009079	AA282120	EST	?
12669	4.9756138651	AA417030	Homo sapiens protein regulating cysteine1 (PRC1) mRNA complete cds	other

FIGURE 3 (cont.)

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29701	4.870526387	H97970	EST	?
20480	4.955753636	NS2168	ESTs	TM
8720	4.9439119502	AA481218	EST - AA481218	other
34828	4.9431269475	AA292436	Homo sapiens senaphoren F homolog mRNA complete cds	SS, TM
14985	4.941621032	U15128	Human beta-12-N-acetylglucosaminyltransferase II (MGAT2) gene complete cds	?
16115	4.937755322	AA004420	ESTs	?
42506	4.9348987118	W70074	EST	other
34761	4.9316837445	AA287833	ESTs	other
11870	4.9281056201	AA262587	ESTs	TM
23211	4.9256381854	T40889	ESTs	other
40611	4.9160502275	N39138	Homo sapiens mRNA for KIA0584 protein partial cds	other
42611	4.9128605354	V87006	Homo sapiens putative RNA binding protein KOC (KOC) mRNA complete cds	other
39652	4.9045174605	HD3099	ESTs	other
17581	4.889674751	AA129395	EST	?
73239	4.8704378349	AA449121	ESTs	?
18712	4.8703618781	F04677	ESTs	other
30709	4.8611171583	N81752	ESTs Weakly similar to synapse-associated protein sap47-1 (G-metagenes)	other
34179	4.8553613848	AA227903	ESTs Highly similar to GTP-BINDING PROTEIN LEPA (Pseudomonas fluorescens)	other
21433	4.825670989	R22183	EST	?
39731	4.8166142741	H11760	ESTs	other
31295	4.8116614607	N56553	ESTs	other
24647	4.804163056	Z39108	EST	?
31282	4.800871617	N86615	ESTs	other
1285	4.7987542393	HG4157-HT4427	EST - HG4157-HT4427	?
1106	4.7932425554	HG2881-HT3127	EST - HG2881-HT3127	?
18212	4.7912282565	AA196506	ESTs	other
34367	4.782207045	AA251758	Homo sapiens spleen mitotic checkpoint1 (BUB3) mRNA complete cds	other
34802	4.7797760205	AA291468	ESTs	TM
34762	4.7775301546	AA287834	ESTs	other
11596	4.7696612848	AA242819	ESTs	other
8296	4.7639639111	AA405082	ESTs	?
17622	4.756633576	AA131584	ESTs Weakly similar to SOF1 PROTEIN (Saccharomyces cerevisiae)	other
35761	4.7572483623	AA405335	ESTs	other
34754	4.7483874972	AA207642	Human mRNA for KIA0078 gene complete cds	?
23237	4.7444654358	T47291	EST	?
37667	4.728044557	AA460318	ESTs Highly similar to 60S RIBOSOMAL PROTEIN L36 (Pisum sativum)	other
11568	4.7257189976	AA28786	ESTs	other
39622	4.7190368733	AA589967	ESTs	?
5137	4.7057389474	U78296	Dihydropyrimidine S-acetyltransferase (E2 component of pyrimidine dihydrogenase complex)	other
25038	4.7002244728	AA010065	COX2B protein kinase 2	other
19288	4.7000147312	H16567	ESTs	other
32503	4.6979488292	T17045	Collagen type I alpha-2	other
3278	4.6953738290	M94055	SODIUM CHANNEL PROTEIN BRAIN II ALPHA SUBUNIT	TM
9696	4.6942061018	L36961	Integral transmembrane protein 1	TM
35400	4.6901390698	AA398591	Homo sapiens putative DNA methyltransferase (DNMT2) mRNA complete cds	other
35246	4.6862691303	AA398367	EST Weakly similar to HSP60 protein (M. musculus)	?
30387	4.6822492271	AA425270	ESTs	other
21509	4.6733072542	R27314	ESTs	other
31381	4.6729672124	N67689	ESTs	other
26723	4.6727694925	AA282781	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP21 (Saccharomyces cerevisiae)	other

FIGURE 8 (cont.)

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36326	4.6703621066	AA425151	Human GAP SH3 binding protein mRNA complete cds	other
17409	4.5688418667	AA112136	EST - RC_AA112136	other
4908	4.5522339635	U67156	Human mitogen-activated kinase kinase 5 (MAP3K05) mRNA complete cds	other
30554	4.5456236328	U49967	ESTs	other
36286	4.54539735	AA489647	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Hydrocortisone coculture]	?
13073	4.5426509458	AA433950	ESTs	other
40435	4.5240181006	N21614	Homo sapiens basic-leucine zipper transcription factor MafK (MAPK) mRNA complete cds	other
14474	4.5226654379	AA509427	ESTs Moderately similar to Hs ALU SUBFAMILY SC WARNING ENTRY III (Hs sapiens)	other
38213	4.515309907	AA498847	ESTs Weakly similar to putative p150 [Hs sapiens]	?
5312	4.5066441198	U90716	Human cell surface protein HCAR mRNA complete cds	SS, TM
24225	4.5041655039	W70325	ESTs	?
35588	4.5006962366	AA401750	EST	?
28739	4.5003199051	H06626	EST	?
7203	4.5782962577	AA053096	EST - AA053096	other
2157	4.5772055959	L41939	Homo sapiens protein-tyrosine kinase EPHB2 (EPH2) mRNA complete cds	SS, TM
32086	4.5661024279	R11610	ESTs	?
6065	4.5648114738	AA314779	ESTs Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR (Hs sapiens)	SS
224	4.5622018969	D13633	Human mRNA for KIAA0065 gene complete cds	other
34006	4.5620980241	AA185761	DNA polymerase gamma	other
36366	4.5557384389	U65477	ESTs	other
34065	4.5537335124	AA195517	ESTs Weakly similar to Hs ALU SUBFAMILY J WARNING ENTRY III (Hs sapiens)	TM
6028	4.5357822097	X66503	Adenylosuccinate synthase	other
4166	4.5032530671	U29463	Cytochrome B561	?
42262	4.5024727522	H83562	ESTs	TM
22687	4.5010672548	R88209	ESTs	TM
41069	4.4977510482	N83969	Hs sapiens mRNA for hFai protein	SS
6284	4.4793100575	AA401334	ESTs	other
27588	4.4720172387	AA443187	ESTs	other
35662	4.4717897552	AA412047	ESTs	?
34479	4.465518191	AA202000	Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA complete cds	TM
15921	4.4546516436	Y12005	Homo sapiens mRNA for nucleolar protein hNcp56	?
11279	4.4380038671	AA195399	ESTs	other
39222	4.4367850786	AA621348	ESTs Highly similar to DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE [Saccharomyces cerevisiae]	other
34428	4.4364738768	AA258526	ESTs	other
8771	4.432067373	AA491186	ESTs	other
22193	4.4189610024	R53951	Homo sapiens mRNA from chromosome 5q21-22 clone: A3-A	other
7886	4.4066170674	AA203032	ESTs	other
19902	4.3886145005	H66736	ESTs	other
9276	4.38608095209	D82374	ESTs	other
10716	4.3794529068	AA053319	ESTs	TM
13193	4.3751913512	AA442763	ESTs Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mus musculus auratus]	other
5690	4.3723059417	X17620	NUCLEOSIDE DIPHOSPHATE KINASE A	other
35102	4.37147138	AA371509	EST - RC_AA371509	TM
17863	4.3612586467	AA169226	ESTs	other
24962	4.3497206925	AFEX-HUMTFRRM11507_5	AFEX-HUMTFRRM11507_5	?
31680	4.3416539659	NT4438	ESTs	other
27168	4.3303080894	AA410258	ESTs	other
28731	4.3231646659	D20961	EST	?
28348	4.3212284906	AA608762	ESTs	other

FIGURE 8 (cont.)

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16335	4 3019961467	AA018587	ESTs Weakly similar to III ALU SUBFAMILY SP WARNING ENTRY III [H.sapiens]	?
33036	4 2915644973	W68560	ESTs Weakly similar to transposon LRE2 reverse transposase homolog [H.sapiens]	other
30180	4 2897721925	N33144	ESTs	other
35581	4 2895541242	AA401755	ESTs Weakly similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	SS
25340	4 2721717135	AA054554	EST	?
28106	4 2658103748	AA485084	ESTs	other
38690	4 2649184307	AA600121	ESTs	other
20253	4 2629499431	H26855	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	other
10251	4 2605750694	R76185	ESTs Weakly similar to C01867 [C.elegans]	SS
12694	4 2604192389	AA417550	ESTs	SS
31636	4 2509469427	N73680	Natural resistance-associated macrophage protein 2	TM
20789	4 2479765348	N87277	ESTs	other
1572	4 2353281083	K01884	EST - K01884	?
10923	4 2292320272	AA115036	ESTs	other
34360	4 2283792392	AA252414	ESTs	other
10132	4 2222816115	R35733	EST - R35733	other
19629	4 2161752119	AA036011	ESTs	other
25146	4 1969683794	AA026356	ESTs	?
28730	4 1965943098	D20959	ESTs Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]	other
10200	4 1874912391	R64521	ESTs	other
38695	4 1545794663	AA600176	ESTs	other
31365	4 150549979	N87550	ESTs	other
42379	4 1496120668	W37899	ESTs	other
28050	4 1428703354	AA479139	Acid phosphatase 1 soluble	other
2620	4 1385565707	M29474	Human recombination activating protein (RAG-1) gene complete cds	?
8827	4 1340593744	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA complete cds	other
13379	4 1282649188	AA448741	ESTs Weakly similar to AF-9 PROTEIN [H.sapiens]	other
8154	4 1218251808	U79293	Human clone 23948 mRNA sequence	other
2626	4 1213948	M29681	Zinc finger protein 6 (clone HF-18)	other
36005	4 1160483666	AA479969	ESTs	other
36575	4 1127196584	AA431085	EST	?
18296	4 1121837207	AA213820	ESTs Weakly similar to putative p50 [H.sapiens]	?
29531	4 1111459313	H08953	EST - RC_H08953	TM
143	4 1085805008	AFEX: HUMTFRRM11507	AFEX: HUMTFRRM11507_5	?
10870	4 0967013395	AA128390	ESTs	other
25636	4 0952825397	AA152305	Interferon (gamma)-induced cell line protein 10 from SS	SS
19735	4 0937927853	H53036	EST	?
40711	4 0903709431	N83564	ESTs	other
4149	4 0901471427	U28385	RAG (recombination activating gene) cohort 1	TM
5767	4 0862764557	X53793	MULTIFUNCTIONAL PROTEIN AGE2	other
5503	4 0861035825	X55232	Stromelysin	SS
20310	4 0641711656	N34693	ESTs Highly similar to HYPOTHETICAL 47.8 KD PROTEIN 80280.9 IN CHROMOSOME II [Caenorhabditis elegans]	other
456	4 0599824566	D38145	Prostaglandin G/H synthase	SS
7814	4 0559685576	AA248406	ESTs	other
40230	4 0447282719	H90161	ESTs	SS
33651	4 038204804	W05409	ESTs	other
16777	4 0231657929	AA048968	EST	?
19110	4 0094005222	H08778	ESTs	other
34442	4 0077010365	AA258093	HKR-T1	other
5099	4 004920433	U79247	Human clone 23598 mRNA sequence	TM

FIGURE 8 (cont.)
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8200	3.9960473163	AA364220	ESTs	other
24408	3.9976866074	W00146	ESTs	other
26596	3.9974919787	AA279943	ESTs	other
16485	3.9811264008	ED26269	Spleen locus forming virus (SFFV) proviral integration oncogene sp1	other
32969	3.9804901745	W02451	ESTs	TM
27006	3.9769768053	AA390695	ESTs Weakly similar to E04F5.2 gene product (C. elegans)	other
29809	3.9526765967	N21043	EST	?
9596	3.9440163451	H91564	ESTs	TM
29024	3.9377933938	F09315	Homo sapiens mRNA for KIAA0563 protein partial cds	other
21694	3.9350368584	R39317	Homo sapiens protein-tyrosine kinase EPHB2v (EPHB2) mRNA complete cds	other
13207	3.929998104	AA443321	ESTs	other
37865	3.9143752629	AA176823	ESTs Highly similar to PUTATIVE UNISQUIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C (Schistosoma mansoni)	other
38201	3.9139828172	AA421164	ESTs	?
8961	3.8981160289	AFFX_HUMTFRM11507_3	AFFX-HUMTFRM11507_3	?
17444	3.8927133917	AA115933	ESTs	other
25069	3.8919634527	AA157267	ESTs Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III (C. elegans)	TM
24982	3.89042252	Z14115	ESTs Highly similar to DUNE MORPHOGENETIC PROTEIN 1 PRECURSOR (Mus musculus)	other
28685	3.889363206	AA281950	ESTs	?
42300	3.8890230396	T95850	ESTs	?
6495	3.8830844863	X32715	Zinc finger protein 74 (Ces2)	other
38604	3.8828045842	AA598803	ESTs	TM
38368	3.8826713710	AA425756	ESTs	other
30560	3.873278445	N49284	MYB PROTO-ONCOGENE PROTEIN	other
14413	3.8724486158	AA600150	ESTs	other
23823	3.8574624967	T91805	Homo sapiens mRNA for ST1C2 complete cds	other
38158	3.853098938	AA467021	EST	?
2572	3.8518747554	M27281	Vascular endothelial growth factor	other
40100	3.8484168967	H75923	Laminin receptor (218 kDa)	other
40258	3.8482992993	H93340	ESTs	TM
20944	3.8461621525	N74443	ESTs	other
20411	3.8458400966	N48963	Homo sapiens mRNA for KIAA0689 protein partial cds	other
10345	3.8437714481	AA001963	ESTs	other
31261	3.8431974374	N60240	EST	other
8513	3.8378410994	AA460990	ESTs	other
13877	3.8363409835	AA478604	ESTs	other
40748	3.823562321	N50679	EST	?
14509	3.8152852193	AA609843	ESTs	other
10281	3.8065667331	R80333	ESTs	other
25284	3.8044158642	AA045074	ESTs Weakly similar to S2 AD S5-AR1a autoantigen (H. sapiens)	other
6730	3.7900225129	Y09305	H. sapiens mRNA for protein kinase Dyt4 partial	other
16033	3.7894824022	AFFX_HUMISGF3A/M97935_M8	AFFX-HUMISGF3A/M97935_M8	?
39242	3.7827164808	AA621523	ESTs	other
27354	3.7794760435	AA425221	ESTs	?
4552	3.777263505	H49188	Human placenta (DH33) mRNA complete cds	SS, TM
18285	3.7756199100	AA227219	Homo sapiens CAGF9 mRNA partial cds	other
16754	3.7677416053	AA048067	EST - RC_AA048067	other
12762	3.7671137403	AA421250	ESTs	other
42463	3.7601033106	W60180	ESTs	other

FIGURE 8 (cont.)
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10614	3.7561669016	AA037357	ESTs	?
867	3.745937969	D87746	Human mRNA for KIAA0007 gene partial cds	other
7608	3.7336647135	AA160967	ESTs	other
31795	3.732736742	N80703	ESTs	other
35377	3.7273764603	AA395453	EST - RC_AA395453	?
22828	3.7243925524	R98192	ESTs	other
25240	3.7243198336	AA039713	ESTs	other
11008	3.7197861366	AA134289	ESTs Weekly similar to ASH1 [O.melanogaster]	?
4341	3.7162349944	U38545	Human ARF-activated phosphatidylinositol-specific phospholipase D1a (pPLD1) mRNA, complete cds	other
28833	3.7147818353	U59787	EST - RC_U59787_f	?
3750	3.7121007154	U99279	Collagen type XDK alpha 1	SS
17483	3.6945413512	AA122147	ESTs	TM
16854	3.6915208471	AA055552	ESTs Weekly similar to KIAA0319 [H.sapiens]	TM
3709	3.6851656771	U07550	Heat shock 10 kD protein 1 (chaperonin 10)	other
1809	3.6652978422	L00205	KERATIN TYPE II CYTOSKELETAL 80	?
24577	3.6617721053	Z38727	Homo sapiens mRNA for KIAA0555 protein complete cds	TM
31032	3.6570916386	N82506	ESTs	other
4951	3.6536195433	U69546	Human RNA binding protein Etr-3 mRNA complete cds	other
37660	3.6523276307	AA460225	ESTs	other
20418	3.6495315781	H49209	ESTs	other
27895	3.6485167436	AA470155	Homo sapiens cohesin protein (COP1) mRNA complete cds	?
7971	3.6434397185	AA287423	ESTs	other
27806	3.64303453	AA443793	ESTs	other
24877	3.6427250533	Z39338	ESTs Highly similar to POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR [Mus musculus]	other
11070	3.6405198277	AA145521	ESTs Weekly similar to putative p150 [H.sapiens]	TM
8328	3.6395048599	D89618	Homo sapiens importin-alpha homolog (SRP1gamma) mRNA complete cds	other
38626	3.634689802	AA435996	ESTs	other
17678	3.6300045795	AA134275	Human HDV1 late element modulatory factor mRNA sequence from chromosome 3	other
36209	3.6274894477	AA421256	ESTs Weekly similar to LIS-1 protein [H.sapiens]	other
34120	3.6258800412	AA211616	EST	?
35152	3.62465442011	AA486737	H.sapiens mRNA for Sm protein F	TM
35463	3.6184893268	AA504491	ESTs Weekly similar to contains similarity to C2HC4-class zinc finger [C.elegans]	TM
20064	3.6183899978	H98653	ESTs	TM
31296	3.5992620732	N86152	EST	?
6713	3.5965226843	L44338	Homo sapiens mRNA for KIAA0525 protein partial cds	other
26822	3.5768056147	D11837	ESTs	?
38057	3.5736106703	AA491549	EST - RC_AA491549	other
28763	3.5688723791	D45568	EST	?
16996	3.5680705709	AA069038	EST - RC_AA069038	TM
26828	3.5604144617	D11868	ESTs Moderately similar to PROHIBITIN [H.sapiens]	?
25804	3.5442954572	AA148885	ESTs	?
2492	3.5423964239	C28288	Tumor protein p53 (Li-Fraumeni syndrome)	?
14904	3.5411970737	T83389	ESTs Highly similar to GEPHYRIN [Rattus norvegicus]	other
25205	3.5347588502	AA043765	H.sapiens RY-1 mRNA for putative nucleic acid binding protein	other
13606	3.53277912417	AA456437	ESTs Weekly similar to CLEAVAGE STIMULATION FACTOR 64 KD SUBUNIT [H.sapiens]	other
42307	3.5316436465	T90595	EST - RC_T90595	TM
1544	3.528202414	J05068	TRANSOCALAMIN I PRECURSOR	SS
42338	3.5195061035	W02072	ESTs Weekly similar to No definition line found [C.elegans]	other
42311	3.5183719631	T97267	ESTs	other
2023	3.5040279423	L34800	MITOCHONDRIAL PRECURSOR	other

FIGURE 8 (cont.)

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4540	3 4955305569	U45807	Human MAP kinase phosphatase (MKP-2) mRNA complete cds	other
33707	3 4888534277	Z38297	Neuronal pentraxin II	other
17220	3 4755763461	AJ083070	EST - RC_AA080070_s	SS
24332	3 4725273805	W85782	ESTs	other
35887	3 4666063718	AA112067	ESTs	other
20158	3 4538150055	N23638	ESTs Weakly similar to coded for by C. elegans cDNA y62a10.5 [C.elegans]	other
8338	3 4465832071	AA417152	Homo sapiens protein regulating cytokinesis 1 (PRC1) mRNA complete cds	other
387	3 4421627234	D25589	EST - D25589	other
12319	3 4356289717	AA388109	ESTs	SS, TM
38276	3 4313139432	AA485711	ESTs	TM
15643	3 4212194246	W58247	ESTs Highly similar to KINESIN-LIKE PROTEIN KIF4 (Mus musculus)	other
11218	3 4232932843	AA180488	ESTs	TM
16539	3 417866379	AA020328	Human mRNA for KIAA0073 gene partial cds	?
29203	3 4162847487	H28581	ESTs	other
13838	3 4162403464	AA465342	ESTs	other
25585	3 4160330303	AA112388	H4(D10S170)	SS
34018	3 4145335583	AA191486	Human high-affinity copper uptake protein (hCTR1) mRNA complete cds	TM
251	3 4006942851	D14520	Basic transcription element binding protein 2	other
3778	3 4004516201	U09848	Zinc finger protein 139 (clone p142-37)	other
24535	3 3964337637	Z38409	ESTs	other
16658	3 3825194041	AA055759	Human mRNA for KIAA0128 gene partial cds	TM
16127	3 3821645297	AA004669	ESTs	other
36683	3 3641315491	AA432288	ESTs	other
26149	3 3809497785	AA350824	ESTs Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]	other
4011	3 3788093471	U20536	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
41001	3 3784250205	N78844	ESTs	other
5660	3 3769336731	X16396	NAD-DEPENDENT METHYLENE-THETRAHYDROFOLATE DEHYDROGENASE	SS
19204	3 3776332343	H11629	ESTs	other
42323	3 3766515979	T90152	Fibillin 2	SS
26928	3 3728378666	AA342560	ESTs	SS
20497	3 3692859112	N52565	ESTs	other
19226	3 36674248	H12455	ESTs	other
36267	3 3606641838	AA424046	ESTs	other
32257	3 3589796018	R54726	DNA-REPAIR PROTEIN KRCC1	other
17365	3 3522214732	AA101551	ESTs	other
15296	3 34491193196	W16684	ESTs Moderately similar to Similar to S. cerevisiae hypothetical protein L3111 [H.sapiens]	other
17675	3 3485870272	AA134064	ESTs	TM
40332	3 3456486599	H97565	Homo sapiens mRNA from chromosome 5q21-22 clone A3A	other
7219	3 3365684543	AA056319	Homo sapiens protein phosphatase 2A B56-epitkin (PP2A) mRNA complete cds	other
10006	3 3322827822	N81193	Homo sapiens mRNA for KIAA0628 protein complete cds	?
33885	3 3276877441	AA101560	Homo sapiens importin beta subunit mRNA complete cds	other
9570	3 3283553302	H85169	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene complete cds	other
37551	3 3150406577	AA456678	ESTs	other
886	3 3111782759	D80613	Human mRNA for hQDMA complete cds	other
23650	3 3069426629	T86253	ESTs	other
16367	3 3007433533	AA224180	ESTs Moderately similar to ovarian specific protein [R. norvegicus]	?
42494	3 2908070546	W65385	H.sapiens NIMA gene (Clone T33)	other
14310	3 2753564661	AA58412	ESTs Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN PM76-PCT INTERGENIC REGION [Saccharomyces cerevisiae]	SS, TM

FIGURE 8 (cont.)

19233	3.274416299	H12634	ESTs	other
42283	3.2731086204	T94343	Homo sapiens M952 protein spliced isoform 2 mRNA complete cds	other
12809	3.271352097	AA434406	ESTs	other
36285	3.2696023617	AA434469	ESTs	other
21555	3.2668296446	R33073	EST	?
19767	3.2655595616	AA463234	ESTs	TM
4738	3.2661591937	U58766	Human FX protein mRNA complete cds	other
7256	3.263109966	AA075427	ESTs	other
17041	3.2629042076	AA070364	EST - RC_AA070364	?
15504	3.2616745245	W08362	ESTs	other
23793	3.2611826986	T00971	EST - RC_T00971	other
18214	3.2572346955	AA196635	ESTs	TM
7401	3.2571641233	AA094800	Human translation initiation factor eIF3 p86 subunit mRNA complete cds	other
18912	3.2553600001	F10913	Homo sapiens clone 22617 unknown mRNA partial cds	other
36317	3.25509495347	AA425009	Human mRNA for KIAA0534 gene complete cds	?
9410	3.2507279651	H20443	H. sapiens mRNA for TRES	other
2146	3.2464307696	L41390	EST - L41390	?
18663	3.240614336	F04258	ESTs Highly similar to INORGANIC PYRIPHOSPHATASE (Boa tauru)	?
33891	3.2392191408	AFFX: HUMTFRFRM115 07	AFFX-HUMTFRFRM11507_M	?
14435	3.2372161315	AA608730	ESTs Weakly similar to ELONGATION FACTOR 1-ALPHA [Gianta ensa singali]	other
8504	3.2365629855	H86128	ESTs Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]	other
22061	3.2340099572	R49216	ESTs	TM
35796	3.233287665	AA102223	EST - RC_AA102223	?
37403	3.2261652043	AA453613	ESTs	other
15796	3.2260359988	X16889	ALPHA-GALACTOSIDASE A PRECURSOR	SS
15840	3.2257932430	X70944	PTB-ASSOCIATED SPLICING FACTOR	other
7518	3.2252170427	AA147144	EST - AA147144	other
32335	3.2228368992	R78248	ESTs	other
3256	3.2180538038	M92439	130 KD LEUCINE-RICH PROTEIN	other
4400	3.2173694081	U41367	Human Gu protein mRNA partial cds	other
7081	3.2074414289	AA320683	Homo sapiens mRNA for DRIM protein	other
15676	3.2041299443	V68649	ESTs	TM
35690	3.2036956821	F09051	ESTs	other
26683	3.1980022253	AA291921	ESTs Weakly similar to putative p150 [H.sapiens]	?
9608	3.1920360354	M90627	Transcription factor 12 (TF14 helix-loop-helix transcription factors 4)	other
27755	3.1900699454	AA453444	ESTs	other
29863	3.1882280623	K26011	ESTs	?
21350	3.1876957756	R15946	ESTs	other
11981	3.1870525747	AA280528	ESTs	other
23930	3.1817500097	T96690	ESTs Weakly similar to 1H ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
30299	3.1792054412	H45226	EST	?
22286	3.1781990049	R59312	ESTs	other
13494	3.1673900969	AA453431	ESTs	TM
12608	3.1530033441	AA427579	ESTs	other
22319	3.1469419301	R60567	ESTs	TM
31309	3.1468750623	N56818	ESTs	TM
31192	3.1458779823	N64406	ESTs	other
11288	3.144853134	AA195912	ESTs	TM
170	3.1430726349	D00596	Thymidylate synthase	?
5307	3.1340705478	U90549	Human non-histone chromosomal protein (H4C) mRNA complete cds	other

FIGURE 8 (cont.)

26105	2 1311103325	AA243133	Homo sapiens serine/threonine kinase (BTAK) mRNA complete cds	other
11659	2 1201786108	AA251909	Homo sapiens MAD3-like protein kinase mRNA complete cds	other
19177	3 124408565	H10984	ESTs	TM
8389	3 1241545024	AA425230	ESTs	TM
34097	3 1216555797	AA205125	Protein serine/threonine kinase ssk2	other
25001	3 1209327466	AA004710	ESTs Weakly similar to BAP31 protein [H.sapiens]	other
14149	3 1185000308	AA489665	ESTs	other
10167	3 1181986523	RS5078	ESTs	other
17390	3 1071065866	AA102566	ESTs	other
42397	3 1044680628	W42928	ESTs	other
14935	3 1042015743	T94628	ESTs Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]	other
41873	3 1030349619	R78618	ESTs Weakly similar to GTP-binding protein rab10 [R.novgorodensis]	other
2750	3 1028223619	M35999	Integrin beta 2 (platelet glycoprotein IIb antigen CD61)	?
3190	3 1026225619	M66006	PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT TESTIS-SPECIFIC FORM PRECURSOR	?
17406	3 0999394188	AA112979	Homo sapiens mRNA for VRK1 complete cds	other
598	3 0912414004	D59253	Homo sapiens mRNA for low molecular mass ubiquitinone-binding protein complete cds	other
29346	3 0902365759	H59021	ESTs	other
14130	3 0744457534	AA489041	ESTs	other
14134	3 069660341	AA489000	ESTs Highly similar to phosphorylation regulatory protein RFP-10 [H.sapiens]	other
42421	3 0664159011	W45491	ESTs Weakly similar to T23G11.7 [C.elegans]	other
15723	3 0660746209	W79060	ESTs Highly similar to ribosome-binding protein p34 [R.novgorodensis]	other
11140	3 0650815188	AA158132	ESTs Highly similar to YSA1 PROTEIN [Saccharomyces cerevisiae]	other
20531	3 0649787887	C30679	ESTs	other
2021	3 0628707497	L34409	Homo Sapiens (clone B3B3E12) chromosome 4p16.3 DNA fragment	?
14822	3 0582801853	AA810108	ESTs Highly similar to PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C11E11.05C [Schistosoma mansoni]	SS,
29553	3 0545021015	N22182	ESTs	other
15862	3 0521475703	Z21420	ESTs	other
6541	3 0508006038	X95632	Human Abl Interactor 2 (Abl-2) mRNA complete cds	other
13229	3 0485366337	AA443011	ESTs	other
27315	3 046622812	AA424038	ESTs	other
13621	3 0302305369	AA456821	ESTs Highly similar to BCNE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]	other
39829	3 0269182450	AA412429	ESTs	other
17825	3 0253428426	AA164209	Homo sapiens RRM RNA binding protein Gry-rip (GRY-RRP) mRNA complete cds	other
5053	3 0249530782	U78902	Human Tet-SF1 mRNA complete cds	other
15000	3 0213203848	U54999	Human LGN protein mRNA complete cds	other
17757	3 0205801351	AA147224	EST	?
19050	3 0182379314	H05508	ESTs	other
20630	3 0176822370	AA278650	ESTs	other
16806	3 0158779932	AA052258	Homo sapiens mRNA for KIAA0648 protein partial cds	TM
23088	3 0149440394	F13700	Homo sapiens ribonuclease P protein subunit p40 (RPP40) gene complete cds	other
22960	3 01418662421	T10272	ESTs	other
33585	3 0121672451	W63000	ESTs	other
220	3 0109180714	D13627	Human mRNA for KIAA0002 gene complete cds	TM
4298	3 0024571064	U36448	Human Ca2+-dependent activator protein for secretion mRNA complete cds	TM
7445	2 9995043641	AA104023	ESTs	?
40903	2 9990347060	N68670	ESTs	?
19055	2 9973386648	AA179387	ESTs	other
7282	2 9962792596	AA083309	ESTs	other

FIGURE 8 (cont.)

9348	2.994901671	H03686	ESTs	TM
806	2.937478515	D87009	Human (lambda) DNA for immunoglobulin light chain	?
39447	2.9876031644	AA504255	Human protein kinase ATR mRNA complete cds	other
41464	2.987604981	R46837	ESTs	?
9662	2.9899352306	L19161	TRANSLATIONAL INITIATION FACTOR 2 GAMMA SUBUNIT	other
16976	2.9891154057	AA03625	EST	?
37426	2.975640806	AA454016	ESTs	other
2588	2.9725698298	M27878	Zinc finger protein 84 (HPF2)	other
15174	2.9695024379	U82987	Human Bcl-2 binding component 3 (bcl3) mRNA partial cds	other
33620	2.9687440567	W59343	ESTs	other
6784	2.965506112	Y11681	Homo sapiens ribosomal protein S12 gene nuclear gene encoding mitochondrial protein complete cds	?
41077	2.9642389716	N19508	ESTs	TM
1932	2.9609955995	L24604	Human (g23) mRNA complete cds	other
39586	2.9588964022	F03738	ESTs	other
16108	2.9574232912	AA002258	ESTs	SS,
32156	2.9574232912	R40381	ESTs	?
13617	2.9552305938	AA456646	ESTs	other
11889	2.955203991	AA281251	ESTs Weakly similar to thorax protein trill (D.melanogaster)	other
6256	2.947654132	X58194	Pseudovirus (human keratinocyte line HaCaT mRNA 2106 nt)	TM
15440	2.9445492866	Y27374	Homo sapiens 10KD protein (BC10) mRNA complete cds	?
38088	2.9445277634	AA482557	EST	?
13878	2.9444133364	AA476604	ESTs	other
6309	2.9422425032	X76770	H.sapiens PAP mRNA	other
358	2.9337591919	D28791	Phosphatidylinositol glycan class A (paracatalin) (normal hemoglobinuria)	?
1351	2.9286145862	H04755-HT5203	EST - H04755-HT5203	?
42624	2.9286145862	W87804	ESTs	other
34895	2.9242794509	AA311972	ESTs	other
20167	2.9214162876	N23393	ESTs	other
28240	2.9188102156	H52816	ESTs	?
4893	2.9175533564	U60615	Human SWI5NF complex 155 KDa subunit (BAF155) mRNA complete cds	other
10104	2.9150324084	R23055	ESTs	TM
15039	2.9147218324	U46116	Protein tyrosine phosphatase receptor type gamma polypeptide	?
1605	2.9141775797	L00058	V-myc-avian myeloblastosis viral oncogene homolog	?
4536	2.907660336	U48705	Receptor protein-tyrosine kinase EDDR1	?
10173	2.905710598	R56678	ESTs Weakly similar to cell division control protein CDC2 (p34 ^{cdc2})	?
26555	2.9056210172	AA279071	ESTs Weakly similar to TDBA11.2 (C.elegans)	other
4401	2.9047655562	U41515	Human deleted in split hand/split foot 1 (DSB1) mRNA complete cds	other
21008	2.8995011918	H90401	ESTs	TM
3602	2.894817322	U01317	HEMOGLOBIN EPSILON CHAIN	?
4633	2.8919254016	U63455	Sulfonylurea receptor (hypersulfonylurea)	?
36200	2.8912301428	AA421864	ESTs	?
26645	2.8898309441	AA281076	ESTs	other
35259	2.8887681574	AA398622	Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	other
9804	2.8880347444	M74558	Human S1L mRNA complete cds	other
5216	2.8877977515	U83410	Human CUL-2 (cul-2) mRNA complete cds	other
12313	2.8846782103	AA397916	ESTs	other
5628	2.8836080438	X62048	WEE1-LIKE PROTEIN KINASE	?
36586	2.8818258313	F09155	ESTs	TM
34758	2.8775214637	AA287680	EST	?
18199	2.8753640024	AA195318	ESTs	other

FIGURE 8 (cont.)

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19907	2.8720974686	H61476	ESTs	?
6081	2.8670372936	X69398	CD47 antigen (Rb-related antigen integrin-associated signal transducer)	SS, TM
5254	2.862007239	U86782	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	other
13579	2.8570620454	AA455967	Human neuronal PAS2 (NPAS2) mRNA complete cds	?
1117	2.8565053461	HG3075-HT236	EST - HG3075-HT236	?
20033	2.8564878641	N64407	ESTs	TM
35455	2.8562453397	AA505118	Human nucleoporin 98 (NUP98) mRNA complete cds	other
33729	2.8548155651	Z39654	EST	?
2028	2.8532778139	L35035	RIBOSE 5-PHOSPHATE ISOMERASE	other
27374	2.8520674335	AA425816	ESTs Weekly similar to Y53C12A.3 [C.elegans]	other
19404	2.8519690748	H05668	ESTs	other
26108	2.8504706329	AA241989	ESTs	SS,
4189	2.8439972255	U93930	UDP-glucosyltransferase 6 (UDP-glucosyl ceramide glucosyltransferase)	TM
16708	2.8427389072	AA043944	ESTs	other
357	2.8350474214	D20156	Human mRNA for transcriptional activator hSNF2b complete cds	other
25045	2.8315740098	AA236276	ESTs	other
17790	2.8312342777	AA150435	ESTs	other
8059	2.8268722809	AA310957	ESTs Weekly similar to T04A8.11 [C.elegans]	other
40914	2.8279995584	H69220	ESTs	other
27189	2.8263163852	AA110287	H. sapiens mRNA for basic transcription factor 2 34 kD subunit	other
21368	2.8262413945	R16079	ESTs	other
3572	2.8261489131	S87759	Protein phosphatase 2C alpha (human tarantula carcinoma mRNA [3348 nt])	other
11877	2.8259999492	AA262727	ESTs	other
1853	2.8234017306	L05424	CD44 antigen (cell adhesion molecule)	?
24845	2.8131204426	Z39106	ESTs	other
35830	2.8129257031	AA411448	ESTs	TM
4433	2.8114422177	U43279	EST - U43279	?
20151	2.8109454503	N22895	Homo sapiens clone 1400 unknown protein mRNA partial cds	other
38648	2.8084431065	AA598267	EST - RC_AA599267	other
7777	2.8071817929	AA236820	ESTs	other
32845	2.80583194	W31566	EST	?
28258	2.8043634182	AA505133	ESTs	other
6853	2.798263202	Z22951	TRANSCRIPTION FACTOR P65	?
35944	2.7913872906	AA412488	ESTs	?
30648	2.7866523676	N50971	ESTs	?
18965	2.7857482775	H01411	ESTs	TM
8616	2.785444221	AA60007	ESTs	other
14945	2.7838257917	T99006	ESTs Weekly similar to FS052.2 [C.elegans]	other
5375	2.7806657722	AA422160	H. sapiens NAP (nucleosome assembly protein) mRNA complete cds	other
34929	2.7792111121	AA342084	EST - RC_AA342084	other
326	2.7786976435	O21262	Human mRNA for KIAA0035 gene partial cds	other
27057	2.7781218063	AA000988	ESTs	SS,
36292	2.7746002184	AA424513	EST - RC_AA424513	other
6480	2.7735431318	X91788	H. sapiens mRNA for kln protein	other
15424	2.7731675608	W27054	APOLIPOPROTEIN AI REGULATORY PROTEIN-1	other
11602	2.7730818755	AA343007	ESTs	?
18175	2.77056696	AA194730	ESTs	?
25202	2.7696586996	AA034527	EST	?
1681	2.7697545972	L07453	Replication protein A (E. coli RecA homolog RAD51 homolog)	other
14566	2.767984858	AA621122	ESTs	other
25614	2.7633374335	AA115769	ESTs	other

FIGURE 8 (cont.)

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14182	2.760648934	AA490885	ESTs	other
31599	2.7591187958	N72196	EST	other
18253	2.7471964081	AA066370	ESTs	other
6193	2.7442487702	X75092	Regulatory factor (trans-acting) 3	other
22911	2.7433448959	T03865	ESTs	other
35549	2.743246506	AA41274	Homo sapiens RRM RNA binding protein Gry-rip (GRI- RIP) mRNA complete cds	other
35955	2.7389431758	AA412528	ESTs Weakly similar to ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus [Nassif J; nonrepetitive]	other
17642	2.7377607284	AA132903	ESTs Moderately similar to C-1-TETRAHYDROFOLATE SYNTHASE CYTOSOLIC [H. sapiens]	other
6131	2.7371784571	X72841	Human reticuloblastone-binding protein (RbAp46) mRNA complete cds	other
41429	2.7347564467	R44994	ESTs	other
17052	2.7329444181	AA070815	EST - RC_AA070815	?
34243	2.7294147034	AA235050	ESTs	?
22937	2.7294347248	T10065	Homo sapiens TLS-associated protein TASH-2 mRNA complete cds	other
5180	2.7243199196	U82130	Human tumor susceptibility protein (TSG101) mRNA complete cds	other
30837	2.7231409239	N54416	ESTs	other
16243	2.7228028265	AA012902	ESTs	TM
19954	2.7215189495	H80100	ESTs	other
6444	2.720441364	X89750	H. sapiens mRNA for TGF β protein	other
5915	2.7192379481	X61072	Human mRNA for T cell receptor clone IGRA17	SS
6240	2.7186544194	T78627	H. sapiens mRNA for tranilin	?
42116	2.7144176166	T69924	EST - RC_T69924	other
7701	2.7107230468	AA215333	ESTs	TM
17568	2.7096978988	AA128005	ESTs	TM
42534	2.7096014274	W73189	Homo sapiens protein-tyrosine kinase EPHB2 (EPH2) mRNA complete cds	SS, TM
29613	2.708372123	N21111	ESTs	other
38886	2.7067354943	AA069458	ESTs	other
10316	2.7055636457	R86880	ESTs Moderately similar to zinc finger protein [M. musculus]	other
14769	2.7040021865	S54641	HZF-16	other
32861	2.7012196407	V38306	Human mRNA for KIAA0005 gene complete cds	other
35273	2.6971534545	AA368567	ESTs	other
10180	2.696088303	R60100	ESTs	?
32563	2.6955482902	T27697	Human mRNA for KIAA0036 gene complete cds	other
34502	2.6948574449	AA262708	ESTs	TM
13223	2.6912865353	AA443720	ESTs	other
6494	2.6906515739	AA443460	ESTs	other
7776	2.6900717525	AA236771	ESTs	other
10400	2.6896988951	AA007234	ESTs	other
1130	2.6897627619	HG3132-HT3308	EST - HG3132-HT3308	?
2379	2.6874247447	M16937	Human homeo box c1 protein mRNA complete cds	TM
18906	2.6861450774	F10869	Human S15 domain-containing protein SH3P16 mRNA complete cds	?
34786	2.6853510115	AA291259	ESTs	TM
41955	2.6821406177	T33311	Neuronal pentraxin II	other
2009	2.6791001739	L33881	Protein kinase C δ iso	?
33688	2.6775081286	Z38501	ESTs Weakly similar to PROBABLE E5 PROTEIN [Human papillomavirus type 58]	other
1385	2.6771402807	HG884-HT884	EST - HG884-HT884	?
24758	2.6756080668	Z40075	ESTs	other
7820	2.6742248913	AA192484	ESTs Weakly similar to MITOCHONDRIAL INNER MEMBRANE PROTEINASE SUBUNIT 2 (S. cerevisiae)	other
30733	2.6739544406	N52078	Homo sapiens mRNA for KIAA0637 protein complete cds	other
21256	2.6723253055	R09195	Homo sapiens mRNA for KIAA0564 protein partial cds	other
40528	2.669020458	N29325	ESTs Highly similar to 47 KD PROTEIN (Pseudomonas)	other

FIGURE 8 (cont.)
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			[chlorophylls]	
25285	2.6684545408	AA045083	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	other
9296	2.6678495332	D02775	ESTs Weakly similar to unknown [S.cerevisiae]	SS
12174	2.6669305328	AA029120	ESTs	other
38357	2.6652770538	AA491265	EST	TM
3154	2.6619598906	M83712	Cholinergic receptor nicotinic alpha polypeptide 5	TM
7363	2.655440730	AA038634	ESTs Weakly similar to HYPOTHETICAL 16.8 KD PROTEIN IN SMY2-RP5101 INTERGENIC REGION [S.cerevisiae]	other
1923	2.6530372325	L23808	Matrix metalloproteinase 12 (macrophage elastase)	SS
24906	2.6527048053	Z41540	ESTs	other
34726	2.6495430564	AA027278	ESTs	SS
30407	2.6495430564	N45983	ESTs	TM
20408	2.6450891347	N48787	ESTs Moderately similar to III ALU SUBFAMILY SC WARNING ENTRY III [H.sapiens]	other
7158	2.6450891455	AA037206	ESTs	TM
26286	2.6445109706	AA253551	ESTs	?
19822	2.6431968212	H50664	ESTs	?
12379	2.6428192541	AA399418	Human sapiens mRNA for JM23 protein complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and L146411013307) (R2PD Berlin)	other
22698	2.6396306055	R89287	ESTs	other
24161	2.6384522284	V58015	ESTs	other
9558	2.6370149706	H81487	ESTs	TM
18104	2.6356767288	AA188801	ESTs	other
24862	2.6337246859	Z41563	ESTs	other
40038	2.6347974794	H69485	ESTs	other
8865	2.6344845492	AB002359	Human mRNA for KIAA0361 gene KIAA0361 protein	other
22148	2.6298820965	R51831	ESTs	other
4627	2.6277060831	U51990	Human hPp18 mRNA complete cds	other
8394	2.6275394634	AA425156	ESTs	TM
20422	2.6272599716	N49300	ESTs	other
41502	2.6268613824	R67258	ESTs Moderately similar to rhodokin [M.musculus]	other
612	2.6257836682	D63480	Human mRNA for KIAA0146 gene partial cds	TM
4821	2.619521444	U62801	Human protease M mRNA complete cds	SS, TM
16807	2.617722828	AA053296	ESTs	other
15288	2.6173887018	V07562	ESTs Moderately similar to rAB [R.norvegicus]	other
38023	2.6135617291	AA481066	ESTs	other
23822	2.6120077647	T91715	ESTs Highly similar to HYPOTHETICAL 103.8 KD PROTEIN IN COX5B-PP26 INTERGENIC REGION [Saccharomyces cerevisiae]	TM
10081	2.6116016518	AA128719	ESTs	other
6150	2.6113960679	X74262	RETINOBLASTOMA BRIDGING PROTEIN P48	other
39336	2.6109987712	Z20945	ESTs Highly similar to HYPOTHETICAL 84.2 KD PROTEIN IN CDC12-ORC3 INTERGENIC REGION [Saccharomyces cerevisiae]	other
17793	2.6102158178	AA150242	ESTs Highly similar to modulator recognition factor 2 [H.sapiens]	other
26891	2.6085107387	AA292659	ESTs	other
2175	2.607468376	L42821	Human sapiens Lx-9 mRNA complete cds	TM
10642	2.6048724507	AA040149	Human Chromosome 16 BAC clone CIT9873K-A-27D01	other
15026	2.6031453592	U41816	Human C-1 mRNA complete cds	other
7699	2.6019047419	AA215299	Human sapiens chromosome 19 cosmid R30783	other
6543	2.6011808937	X95654	Human sapiens mRNA for SGP-1 complete cds	other
20638	2.5993564878	M62122	ESTs	other
11308	2.5993311575	AA207114	ESTs	other
4086	2.596362866	U24704	Human endocrine factor-1 mRNA complete cds	other
38615	2.5963096726	AA089838	EST - RC_AA588938	other
11819	2.5961501969	AA258189	ESTs	other

FIGURE 8 (cont.)

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37433	2.5957446266	AA454103	ESTs	other
38270	2.5939657629	AA521186	ESTs	TM
5587	2.5932336399	X13482	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A'	other
19841	2.5930132063	H59617	ESTs Highly similar to LUBQUIN-CONJUGATING ENZYME E3-17 KD [Drosophila melanogaster]	other
10655	2.5925442731	AA040882	ESTs	?
14053	2.5899326477	AA485147	ESTs Highly similar to HYPOTHETICAL 83.6 KD PROTEIN P0202.2 IN CHROMOSOME III [Caenorhabditis elegans]	other
31574	2.5883094453	N71300	EST	?
7614	2.5870699315	AA187579	ESTs Weakly similar to Yee007a-ap [S. cerevisiae]	other
37971	2.5847445397	AA479195	EST	?
7090	2.5845365105	AA009913	Homo sapiens diphthamide biosynthesis protein-2 (DPT2) mRNA complete cds	other
17852	2.5841100415	AA156360	ESTs	other
24219	2.5823379094	W61990	ESTs	other
19070	2.5813845258	H05970	Human clone 23960 mRNA sequence	other
17719	2.5803606155	AA136569	EST	?
36669	2.579196791	AA599694	Human mRNA for KIAA0733 gene complete cds	TM
20982	2.5783857078	N78655	ESTs	TM
9158	2.5731838907	D31446	Homo sapiens breakpoint cluster region protein 1 (BCRCL1) mRNA complete cds	other
11382	2.5731137778	AA227261	ESTs	other
8613	2.5723119462	AA459555	Homo sapiens mRNA for KIAA0649 protein partial cds	TM
13886	2.5716997844	AA476319	ESTs	SS
10923	2.5712815907	R86178	Alaxia telangiectasia mutated (includes complementation groups A C and D)	?
22299	2.567916035	R59601	EST	?
18257	2.5673499508	AA066591	EST - RC_AA066591	other
20555	2.5665424268	N55166	ESTs	other
38552	2.5645918108	P03905	PUTATIVE 60S RIBOSOMAL PROTEIN	other
27530	2.5631130948	AA438999	ESTs	other
1705	2.5608471476	L13434	Human chromosome 3p21.1 gene sequence complete cds	?
14746	2.5603154966	D60354	Human mRNA for KIAA0007 gene partial cds	other
2993	2.5587819672	M64929	Protein phosphatase 2 (formerly 2A) regulatory subunit B (PR 52) alpha isoform	other
19191	2.5545280975	H11297	ESTs	other
12986	2.5507999853	AA430032	ESTs Moderately similar to PTTG gene product (R. norvegicus)	?
16452	2.5488633884	W27451	Human Cdc5-related protein (PCDC5RP) mRNA complete cds	other
18003	2.5485667172	AA171692	ESTs	other
24188	2.5481854467	W67524	Human protein-tyrosine phosphatase (HU-PP-1) mRNA partial sequence	TM
42653	2.5447620627	W62703	ESTs	other
26446	2.5441061071	AA58706	EST Weakly similar to putative p150 [H. sapiens]	?
30438	2.5385548574	N47204	ESTs Weakly similar to C50F4.12 [C. elegans]	other
36365	2.5362912735	AA425893	ESTs Weakly similar to probable CBP3 protein homolog [C. elegans]	other
26135	2.535658968	AA433765	ESTs	other
41885	2.5349932888	T23449	ESTs Moderately similar to ZNF127-Xp [H. sapiens]	SS
15457	2.5343489568	W27460	ESTs	other
27748	2.5320787519	AA631159	Human kinesin-like spindle protein HKSP (HKSP) mRNA complete cds	other
32315	2.5320297999	R69840	ESTs Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (Nucleobac coucang)	?
25310	2.5274401579	AA046745	ESTs	other
42720	2.5222453766	Z39436	ESTs	other
12839	2.5200945911	AA428204	ESTs	other
30746	2.5198420898	N52243	ESTs	?
2222	2.5193624578	L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PPP2A) mRNA complete cds	?
11609	2.5191765545	AA433303	ESTs	TM

FIGURE 8 (cont.)

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9658	2.5185814336	L16991	Docosahexaenyltransferase	other
12210	2.5172044681	AA293774	ESTs Weakly similar to PROBABLE TRYPTOPHAN-TRNA SYNTHETASE MITOCHONDRIAL (C.elegans)	other
3563	2.5169918533	S63364	EST - S63364	other
42407	2.5128230047	W44768	Homo sapiens nephrinocystin (NPH1) mRNA partial cds	?
32826	2.5128052161	W0201	Human mRNA for kinase-related protein partial cds	other
9692	2.5119977118	L37747	LAMIN B1	?
27862	2.5094571267	AA458908	ESTs	TM
33691	2.509267494	Z36630	EST	other
17288	2.5088624644	AA085178	ESTs	SS
9888	2.5076170902	N35449	ESTs Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION (Saccharomyces cerevisiae)	other
5932	2.5073880885	X52153	Mitochondrion maintenance deficient (S. cerevisiae) 3	other
15885	2.5053862632	X56073	H.sapiens mRNA for transfer associated protein X	other
17952	2.5049193223	AA165677	ESTs Weakly similar to F16A11.1 (C.elegans)	other
12197	2.5042458391	AJ293206	ESTs	other
6210	2.5042034456	X76942	Homo sapiens pdgfra-245 mRNA complete cds	other
34047	2.5041917773	AA194196	ESTs Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (H.sapiens)	other
16929	2.5034461307	AA058952	ESTs	other
26834	2.5028075682	AA287138	ESTs Weakly similar to ASPARTYL-TRNA SYNTHETASE (Thermus aquaticus thermophilus)	other
5157	2.5017270256	U00304	Human mitochondrial intermediate peptidase precursor (MPEP) mRNA mitochondrial gene encoding mitochondrial protein complete cds	other
38434	2.5005880072	AA497013	ESTs	?
33269	2.5000262771	W72967	ESTs	other
28891	2.4990009911	AA388284	ESTs	other
7590	2.4948756163	AA173505	ESTs Weakly similar to HYPOTHETICAL 46.1 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION (S.cerevisiae)	other
14960	2.4896232864	U05237	Human fetal A2-50-reactive clone 1 (FAC1) mRNA complete cds	other
13585	2.4886752902	AA455899	ESTs Highly similar to NEUROLYSIN PRECURSOR (Sus scrofa)	other
35901	2.4847673156	AA412151	ESTs	other
38185	2.4826740426	AA487808	Homo sapiens mRNA for KIAA0608 protein complete cds	other
34678	2.4824371274	AA284744	Annealing 30 (56kD subunit)	other
1424	2.4811113231	J02645	Eukaryotic translation initiation factor 2A	other
18778	2.4806222256	AA047008	ESTs	other
21876	2.4789005023	R43286	EST - RC_R43286	?
17779	2.4695728499	AA149641	ESTs	other
24559	2.4682754649	Z38588	ESTs	other
7781	2.467947166	AA429504	Homo sapiens proline-rich G1a protein 1 (PRGP1) mRNA complete cds	?
7474	2.4677129013	AA126592	ESTs Weakly similar to No definition line found (C.elegans)	other
34280	2.4675279697	AA236265	ESTs	other
5316	2.4673813483	U09005	Human clone 23674 mRNA sequence	TM
10218	2.4645965539	R08804	ESTs Highly similar to HYPOTHETICAL 44.2 KD PROTEIN IN SCD2-MRP1 INTERGENIC REGION (Saccharomyces cerevisiae)	other
18106	2.4634292267	AA188981	Homo sapiens neurotactinoma-associated protein HEC mRNA complete cds	?
6465	2.4613516897	X82098	H.sapiens mRNA for transmembrane protein mp24	SS, TM
34954	2.4591845976	AA342389	EST - RC_AA342359	?
42558	2.4588630205	W74751	ESTs	other
27444	2.4585760563	AA430160	ESTs Weakly similar to F25H9.7 (C.elegans)	other
21284	2.4582500599	R10301	EST	?
8920	2.4568596729	AF000265	Homo sapiens cancer associated surface antigen (RCAS1) mRNA complete cds	other
20037	2.4544454116	H27439	ESTs	TM
27602	2.4527990177	AA443702	ESTs Weakly similar to W02B12.7 (C.elegans)	TM

FIGURE 8 (cont.)

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3390	2.4525517032	S59104	RYK receptor-like tyrosine kinase	TM
25040	2.452352841	AA010188	ESTs	other
37713	2.4487800271	AA461317	ESTs	other
40477	2.4477600739	N24005	Homo sapiens BAC clone RG300E22 from 7q21-q31	other
29382	2.4470532391	H72914	ESTs	other
35521	2.4465885249	AA400831	ESTs	other
20324	2.4464518504	N35406	Phospholipase C beta 4	SS
18620	2.4460334993	F02506	ESTs	other
21087	2.4406971835	R00186	EST	?
9500	2.4398301157	N71503	ESTs	other
31905	2.4363228422	N83629	ESTs	SS
15120	2.43456895403	U73524	Human putative ATPGTP-binding protein (HEAB)	TM
26813	2.4339770686	D59257	mRNA complete cds	other
36082	2.4285434916	AA482294	Human C-1 mRNA complete cds	other
34723	2.428289395	AA287115	ESTs	other
7960	2.427332589	AA285277	Homo sapiens brain expressed ring finger protein mRNA complete cds	other
18073	2.4231729031	AA180453	EST	other
36755	2.4222443392	AA435688	EST - RC_AA435688	other
18827	2.4187841215	F11087	ESTs	other
3457	2.4186224787	S74728	Arlequin	TM
38606	2.4177693475	AA598844	ESTs	other
20967	2.41519947	N76086	ESTs	other
24752	2.4141496374	Z40012	Homo sapiens mRNA for KIAA0587 protein complete cds	other
26443	2.4139574256	AA621611	ESTs	?
452	2.4135942278	D20076	RAN binding protein 1	other
11701	2.4134085351	AA253031	Homo sapiens RRM RNA binding protein GRY-1 (GRY-RBP) mRNA complete cds	other
13655	2.412509306	AA458019	ESTs Weakly similar to 26S proteasome subunit p4.5 [H.sapiens]	other
24522	2.4119066031	Z40956	ESTs	other
12672	2.4112720798	AA417067	ESTs	other
4836	2.4105618618	U63747	Human osteoclast stimulating factor mRNA complete cds	other
42200	2.4083628799	T83729	EST - RC_T83729	?
10987	2.4078548868	AA132239	ESTs Highly similar to HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]	other
35672	2.4073821434	AA404995	EST - RC_AA404995	other
6224	2.406310553	X77748	Glutamate receptor metabotropic 3	TM
28395	2.404213441	AA810054	ESTs	other
36390	2.4032864297	AA426291	ESTs Weakly similar to No division line found [C.elegans]	other
21045	2.4031906697	N93403	ESTs	?
4558	2.4024850999	U49379	Human diacylglycerol kinase epsilon DGK mRNA complete cds	TM
12916	2.3998506067	AA427745	ESTs	other
20850	2.3988002334	N69514	ESTs Weakly similar to oxidoreductase [H.sapiens]	other
29759	2.3886103066	H89972	ESTs	other
36786	2.3871559161	AA435815	Human CLK-associated RS cyclophilin CARS-Cyp mRNA complete cds	other
31942	2.3847415736	N93185	ESTs	other
7097	2.38382714	AA011452	ESTs	other
39482	2.3836147708	D50063	ESTs	other
14420	2.3819915706	AA600322	ESTs Highly similar to AAC-RICH MRNA CLONE AAC3 PROTEIN (Eidysostomum discoidium)	other
34629	2.3816035475	AA282527	EST - RC_AA282527	other
27431	2.38054683084	AA429038	ESTs	TM
6367	2.3804071656	X85372	H.sapiens mRNA for Sm protein F	other
11342	2.3802175276	AA223874	Homo sapiens mRNA for KIAA0704 protein partial cds	other

FIGURE 3 (cont.)

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1497	2.38636765	J04508	Topoisomerase (DNA) II alpha (170kD)	other
9841	2.3841922016	M05724	Carcinoma autoantigen C	other
11454	2.3820201875	AA333854	ESTs	TM
29950	2.3807499489	H24902	Homo sapiens mRNA for E1B-55kDa-associated protein	TM
8396	2.3807189729	AA426176	ESTs Weakly similar to Similar to S. cerevisiae hypothetical protein L3111 [H.sapiens]	other
32978	2.3805998259	W42768	Human terminal transferase mRNA complete cds	other
27872	2.3784145648	AA459254	ESTs	other
11623	2.3769685069	AA434617	ESTs	other
26582	2.3766957777	AA279768	ESTs	other
22142	2.3761275381	RS1382	Homo sapiens mRNA for KIAA0559 protein partial cds	other
13633	2.3759355586	AA454907	ESTs Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]	other
11534	2.3747689776	AA326223	ESTs	other
9976	2.3709397882	J54229	DEK PROTEIN	other
6291	2.3688994679	X78121	Choriolsteremia	TM
2362	2.3677644564	M16967	Coagulation factor V	other
22887	2.3673034941	T03314	ESTs	TM
24371	2.3663702815	W87415	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
25296	2.3658134846	AA454261	ESTs	other
9054	2.3647542783	C02472	ESTs Weakly similar to EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR [Homo sapiens]	other
8163	2.3646144577	AA357394	ESTs	other
12233	2.364077771	AA543513	ESTs Weakly similar to LINEgJ H-chain fusion protein (M.musculus)	SS,
22924	2.3634007127	T08195	ESTs	other
14371	2.361524453	AA599219	ESTs Moderately similar to ALR [H.sapiens]	other
12401	2.3607283644	AA400229	ESTs	other
26169	2.3599633162	AA251089	ESTs Weakly similar to ORF YOR261 [S. cerevisiae]	?
23085	2.3592943521	T23539	ESTs Highly similar to zinc finger protein (M.musculus)	other
20524	2.358218239	N53965	ESTs	other
20837	2.3577032216	N66263	ESTs Highly similar to HEXOKINASE TYPE I [Homo sapiens]	other
16201	2.3573132615	AA185396	Homo sapiens DNA sequence from PAC 434Q14 on chromosome 1q22.3-41. Contains the HS01181 gene for hydroxyethyl (11-beta) Dihydrogenase 1 the ADORA2BP adenosine A2b receptor LIKE pseudogene the RIF6	other
7813	2.3566888862	AA248287	ESTs	TM
21196	2.3547018746	R07210	ESTs	other
13377	2.3513919997	AA448720	Homo sapiens clone 24708 mRNA sequence	other
9714	2.3497248732	L44367	ESTs	other
41637	2.3460802052	R58673	ESTs	other
17352	2.34595172	AA100925	ESTs	other
11914	2.3446613991	AA278907	ESTs	?
24890	2.3440589532	Z41634	ESTs	other
26796	2.3434458024	D51272	EST - RC_051272_s	?
36738	2.342525534	AA435870	ESTs Weakly similar to B0564.1 [C. elegans]	other
22491	2.3409294581	R70012	EST	other
4796	2.3403778443	U61538	Human calcium binding protein crip mRNA complete cds	other
40847	2.3397210986	N66364	ESTs	other
15657	2.3392348306	W63827	Small inducible cytokine A5 (RANTES)	TM
24482	2.337404148	Z38137	ESTs	other
42022	2.3336939503	T53138	Homo sapiens mRNA for hTCF-4	TM
36233	2.3314220199	AA469023	ESTs	other
41221	2.33106335624	R21531	ESTs Weakly similar to III ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]	other
8053	2.3297250374	AA300880	ESTs	other

FIGURE 8 (cont.)
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363	2.3275393529	D26528	Human mRNA for RNA helicase complete cds	?
26870	2.3241677574	AA281733	ESTs	other
13407	2.3216524472	AA450200	ESTs	TM
17955	2.3150957398	AA166703	ESTs	TM
31858	2.3150041803	N50600	EST	?
24992	2.3151511584	W42845	Homo sapiens protein tyrosine phosphatase PBR1 mRNA complete cds	SS
16759	2.3118245547	AA046294	ESTs	other
7861	2.3113555404	AJ252436	Homo sapiens clone 23797 and 23917 mRNA partial cds	other
41176	2.3111568749	R05079	Natural resistance-associated macrophage protein 2	TM
3660	2.3104335896	U13913	Homolog of Drosophila slowpoke (potassium channel calcium-activated)	TM
49886	2.3077439929	N68149	ESTs Weakly similar to ERV-INDUCED G PROTEIN-COUPLED RECEPTOR 1 PRECURSOR (Homo sapiens)	other
19428	2.3058992601	H22949	EST	?
36080	2.3048363557	AA417282	EST - RC_AA417282	other
27264	2.3043527378	AA418389	ESTs	other
13600	2.3031966996	AA456296	ESTs	other
13552	2.3026988375	AA454943	ESTs	other
15064	2.3023773291	V67456	ESTs Moderately similar to YY1-associated factor 2 (H sapiens)	?
26583	2.3025403178	AJ279774	ESTs	?
37434	2.3013886299	AA454149	EST	?
7833	2.2992574443	AJ349300	ESTs	other
3674	2.2985613315	U05237	Human fetal A2-50-reactive clone 1 (FAC1) mRNA complete cds	other
33694	2.2984566375	Z38770	ESTs	other
11178	2.2972285082	AA167436	ESTs	?
16977	2.2912855384	AA054616	ESTs	other
19789	2.290119924	H57330	EST	?
5948	2.2900730182	X63337	EST - X63337	?
42097	2.2801548729	T66318	Isoleucine-tRNA synthetase	?
24247	2.2801055891	W73010	Ribosomal protein L37	other
40879	2.2870463837	N67816	ESTs Moderately similar to III ALU SUBFAMILY SX WARNING ENTRY III (H sapiens)	other
5875	2.2850441014	X59405	Membrane cofactor protein (CD46) lymphoblast-lymphocyte cross-reactive antigen	?
22325	2.2850330577	R60777	ESTs	other
9621	2.2844572929	J05032	ASPARTYL-TRNA SYNTHETASE	other
9239	2.2823045248	D79100	ESTs	other
41987	2.2818672358	T47708	ESTs	other
31105	2.28081752	N83207	EST	?
38965	2.2794194837	F04320	Replication factor C 37.4D subunit	other
7404	2.2793872556	AA094989	Homo sapiens voltage dependent anion channel protein mRNA complete cds	other
6388	2.2788670475	X55373	H sapiens mRNA for Sin protein G	other
20263	2.2772934851	N31952	ESTs Moderately similar to HYPOTHETICAL 66.5 KD PROTEIN F02A8.5 IN CHROMOSOME II [Caenorhabditis elegans]	other
14529	2.2722894402	AA620307	ESTs	other
21187	2.2711936864	R07200	ESTs	other
28203	2.2692501412	AA490969	ESTs	other
35320	2.2687130032	AA490611	ESTs	other
41625	2.2680307053	R61933	ESTs	other
4674	2.265734645	U54999	Human LGN protein mRNA complete cds	other
28861	2.2637023919	D60037	EST Weakly similar to C50B8.3 (C.elegans)	other
31052	2.2633040539	N62827	ESTs	other
28756	2.2627797292	AA283832	ESTs	other
11567	2.2614480815	AA236747	Homo sapiens mitogen activated protein kinase activated protein kinase gene complete cds	other

FIGURE 8 (cont.)

25050	2.2605083659	AA011134	ESTs Weakly similar to neuro (H. sapiens)	TM
41905	2.2593192037	T29681	Human serine kinase mRNA complete cds	other
26885	2.2582307009	AA292765	H sapiens mRNA for M-phase phosphoprotein mpp5	other
40505	2.2581890488	N34891	Homo sapiens mRNA for KIA00595 protein partial cds	other
3343	2.2566482074	M19790	SIGNAL TRANSDUCER AND ACTINATOR OF TRANSCRIPTION 1-ALPHA/ETA	other
42435	2.2532463427	Y06994	ESTs	?
5937	2.2489783488	X52534	High-mobility group (prokaryotic chromosomal) protein 2	other
21241	2.2477801609	R08617	ESTs	TM
25756	2.2472586561	AA135968	ESTs	TM
34184	2.2459306213	AA227959	Human cysteine protease Mch2 isoform alpha (Mch2) mRNA complete cds	other
8672	2.2450064129	AA477046	ESTs	other
7387	2.2447544716	AA093877	ESTs	other
28822	2.2424116577	D59352	ESTs	TM
18016	2.2410306445	AA173323	ESTs	other
20843	2.2392887223	N69352	Homo sapiens mRNA for ATP-dependent RNA helicase #46 complete cds	other
10054	2.2387950133	R10266	ESTs Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PHA40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]	other
34094	2.2384164305	AA206008	ESTs	other
41246	2.2360827238	R27296	ESTs	other
22634	2.2346537619	R02637	ESTs	other
19686	2.2319351658	H46502	ESTs	SS
34568	2.2306300547	AA280608	ESTs Weakly similar to K02B2.3 gene product (C. elegans)	other
28446	2.2265709871	AA621752	Human 26S proteasome-associated pad1 homolog (POH1) mRNA complete cds	other
20909	2.2264835116	N71704	ESTs	other
651	2.2260783259	D78129	EST - D78129	SS, TM
40409	2.2244318452	H08877	Homo sapiens exportin 1 mRNA complete cds	other
20340	2.224082527	N30825	ESTs	other
20002	2.2233023294	H93005	EST - RC_H93005	other
37321	2.2208252793	AA451806	ESTs	other
8274	2.2208752623	AA020995	ESTs	other
20221	2.2197714612	N28345	ESTs	other
5792	2.2186001223	X54041	CDG28 protein kinase 1	other
4034	2.218064035	U21858	Human transcription initiation factor TFIIID subunit TAFII31 mRNA complete cds	other
30222	2.2149577590	AA421461	ESTs	other
18567	2.2140926050	AA031591	ESTs	other
4721	2.2134595006	U58046	Human mRNA for KIAA0139 gene complete cds	other
20656	2.2125017907	D19706	Human Qu protein mRNA partial cds	TM
20723	2.2113936194	N66093	ESTs	other
6714	2.2062571749	Y08612	H. sapiens mRNA for Nup88 protein	?
19240	2.205580996	H13205	ESTs	other
36447	2.20500784323	AA428188	ESTs	other
11668	2.202413216	AA252672	Homo sapiens diaphanin biosynthesis protein-2 (DIPK2) mRNA complete cds	other
21650	2.2018153311	R37838	Homo sapiens KIAA0440 mRNA partial cds	other
14152	2.2015953698	AA469790	Homo sapiens Ran-GTP binding protein mRNA partial cds	other
40657	2.1975580207	W02771	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR	other
4642	2.1968027789	U53427	Human RNA polymerase II subunit hRNP187 mRNA complete cds	?
32779	2.1962611079	W02102	ESTs	TM
38341	2.1951559134	AA460967	ESTs	other
11803	2.1921143838	AA267971	ESTs	other
34835	2.190705129	AA292677	ESTs	TM
30085	2.1895604523	AA020599	ESTs	other

FIGURE 8 (cont.)

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4046	2.1877764122	U22376	MYB PROTO-ONCOGENE PROTEIN	?
11500	2.1878723705	AA242868	ESTs Weakly similar to house-keeping protein (Mus musculus)	other
5051	2.1866600566	U76538	Human BRCA1-associated RING domain protein (BRAD1) mRNA complete cds	other
33917	2.1864855739	AA167323	ESTs	TM
20674	2.1856972155	N63392	ESTs	TM
41031	2.1769902734	N91246	ESTs	?
25114	2.1759594688	AA020623	EST	?
34711	2.1758363153	Z39645	ESTs	other
4733	2.1721786534	U56658	Human unknown protein mRNA within the p53 intron 1 complete cds	other
4871	2.1712198791	U66033	Human glyceral-5 (GPC5) mRNA complete cds	other
29733	2.1687028853	H93398	EST	?
23155	2.1678113430	T30550	ESTs	other
34638	2.164515029	AA282087	EST	?
35541	2.1621480372	AA400966	Prothymosin alpha	other
1889	2.1598384252	L20591	Annonin B (lipocortin II)	?
15106	2.1591553963	U68111	PROTEIN PHOSPHATASE INHIBITOR 2	?
40131	2.1583553082	H79779	Homo sapiens histone deacetylase 3 (HDAC3) mRNA complete cds	other
19516	2.158045763	H29207	EST	other
4156	2.1577799237	U28014	ICH-2 PROTEASE PRECURSOR	other
20276	2.1548737104	N32910	ESTs	other
13292	2.1546709291	AA447621	ESTs Highly similar to 40 KD PROTEIN (Borne disease virus)	other
20666	2.154262809	N63165	ESTs	other
6065	2.1526648242	X68560	Sp3 transcription factor	other
18288	2.1516362853	AA205389	ESTs	other
21627	2.1516999194	R37410	EST	?
3438	2.1502571642	S73024	Eukaryotic translation initiation factor 5A	?
34540	2.149893434	AA283772	ACTINATOR 1 36 KD SUBUNIT	other
5964	2.1489964343	X63657	Follicular lymphoma variant translocation 1	SS,
13250	2.1486085975	AA445429	ESTs	other
34370	2.1485846556	AA251829	ESTs Weakly similar to HYPOTHETICAL 27.4 KD PROTEIN IN MER2-CPV INTERGENIC REGION (Saccharomyces cerevisiae)	other
27096	2.145312871	AA470156	ESTs Weakly similar to dyx11 74K chain cytosolic (R. norvegicus)	SS,
4408	2.138886247	U41745	Human PDGF associated protein mRNA complete cds	other
4197	2.1305032136	U30508	Human tRNA-guanine transglycosylase mRNA complete cds	other
10804	2.1306605886	AA099548	ESTs	other
34552	2.1340220702	AA279985	Human mRNA for KIAA0372 gene complete cds	other
16380	2.1331897016	AA227119	ESTs	other
5233	2.1288426563	U83843	EST - U83843	other
37415	2.1270169134	AA453807	EST	other
14582	2.1260941468	AA621340	ESTs Weakly similar to HYPOTHETICAL 39.8 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION (Saccharomyces cerevisiae)	other
27756	2.123647107	AA453447	ESTs	other
13787	2.1232865197	AA63745	ESTs Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 (Saccharomyces cerevisiae)	other
5173	2.1229270565	U81554	Homo sapiens signal recognition particle 72 (SRP72) mRNA complete cds	other
40029	2.1214337319	H68221	Human E2 ubiquitin-conjugating enzyme UbcH5B (UBCH5B) mRNA complete cds	other
19972	2.1193721042	H63639	ESTs	other
23301	2.1179196055	T52847	ESTs	other
20304	2.1134521605	N52966	ESTs	other
40145	2.1132200572	H81391	Human mRNA for histamine N-methyltransferase complete cds	other
3461	2.1131164397	S75256	EST - S75256	SS,
41893	2.1124189285	T23611	ESTs	other

FIGURE 8 (cont.)

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30298	2 1052181318	C14805	EST - RC_C14805	other
30521	2 1064566145	AA16876	ESTs Weakly similar to TRANSFORMATION-SENSITIVE PROTEIN IEF S5P 3521 (H.sapiens)	other
8382	2 1077406838	AA424199	ESTs Weakly similar to CSDB8 3 (C. elegans)	other
28288	2 1075563303	AA598447	Human sapiens exportin t mRNA complete cds	other
5807	2 1071009331	X55740	5' nucleotidase (CD73)	?
19747	2 106109999	H53572	ESTs	other
38155	2 1052355506	AA486777	ESTs	TM
924	2 1037724222	H01112-HT1112	EST - H01112-HT1112	?
9544	2 1022261514	H72630	ESTs	other
8384	2 1005713227	AA424282	Human 75-kD autoantigen (PM-Scl) mRNA complete cds	other
25165	2 1001912894	AA027837	Retinitis pigmentosa 3 (R-linked recessive)	GS, TM
24348	2 1000366838	W65469	Tropomyosin alpha chain (skeletal muscle)	?
41401	2 0994963637	R43334	Human sapiens KIAA0410 mRNA complete cds	other
35340	2 0993762592	AA398900	EST - RC_AA398900	other
10698	2 0990741816	AA112053	ESTs Weakly similar to PRE-MRNA SPLICING HELICASE (SPB2 (S. cerevisiae))	other
381	2 0974305874	D28473	Isoleucine-tRNA synthetase	other
22051	2 0971755	R49047	ESTs Weakly similar to IIIA1J BUBFAMILY J WARNING ENTRY !!! (H.sapiens)	other
3293	2 096563118	MA4593	Taxia specific protein Y-linked	?
11528	2 085454212	AA235018	ESTs Weakly similar to unknown (S. cerevisiae)	?
11890	2 0802855803	AA278323	Human sapiens clone 24506 mRNA sequence	TM
13643	2 0832581265	AA458578	Human sapiens clone 24477 mRNA sequence	other
18927	2 0652547855	H71829	ESTs	other
36511	2 0627695929	AA429632	ESTs	?
2130	2 0525292202	L40407	Human sapiens thyroid receptor interactor (TRIP9) gene complete cds	?
7193	2 0524678877	AA046768	Human sapiens clone TUA8 Cri-du-chat region mRNA	TM
5448	2 0521043187	X02751	Neuroblastome RAS viral (v-ras) oncogene homolog	?
35956	2 0476785163	AA112533	ESTs	other
7525	2 0470133892	AA149259	ESTs	other
39892	2 0462891765	F09251	ESTs Weakly similar to weakly similar to S. cerevisiae PTM1 precursor (C. elegans)	TM
28029	2 0455736844	AA478476	ESTs	other
18425	2 0455157851	AA232103	ESTs	other
23494	2 0443308662	T70045	ESTs Weakly similar to HYPOTHETICAL 33.2 KD PROTEIN P26A3.7 IN CHROMOSOME 1 (C. elegans)	other
30882	2 0403121831	N56906	EST	?
32597	2 0403196473	T47333	Human TFII0 subunit TAF1B5 (TAF1B5) mRNA complete cds	other
33308	2 0403617614	W50614	ESTs	other
10259	2 0403121213	R77527	ESTs	other
21882	2 04025457608	R43365	ESTs	other
20590	2 04020571859	N58146	ESTs	other
12907	2 0401802348	AA427577	ESTs	other
22956	2 0770089467	T10264	ESTs	other
42044	2 0762746251	T56753	ESTs	other
4210	2 0750374179	U31814	Human transcriptional regulator homolog RPD3 mRNA complete cds	other
99	2 074214716	AB003690	Human sapiens mRNA for Cdc7-related kinase complete cds	other
14350	2 0739236064	AA598031	ESTs	TM
29840	2 0729224128	N21680	ESTs	other
25993	2 0715918096	AA113149	Human sapiens IPI (IPL) mRNA complete cds	other
26071	2 0706411247	AA236890	Protein phosphatase 2A regulatory subunit B' alpha-1	other
26529	2 0699045563	AA278594	EST	?
12154	2 0692192056	AA291293	ESTs	other
18817	2 0684614207	F10077	ESTs	?

FIGURE 8 (cont.)

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6635	2.0674931973	X99585	H sapiens mRNA for SMT3B protein	other
6681	2.066065203	Y00971	Phosphoribosyl pyrophosphate synthetase 2	other
22077	2.064745330	R49482	ESTs	other
11752	2.0645929355	AA256042	ESTs	other
41257	2.0634413934	R31690	ESTs	SS
6904	2.0622301932	Z34897	Histamine receptor H1	TM
16879	2.060282971	AA056538	ESTs	other
30040	2.0595448235	AA481403	ESTs	other
4111	2.0567536207	U25312	Human heterochromatin protein HP1b gamma mRNA complete cds	other
32878	2.0546812272	W07448	ESTs	TM
21743	2.0543668440	R40370	ESTs Moderately similar to IRI ALU SUBFAMILY SX WARNING ENTRY IRI [H sapiens]	?
23958	2.0525016401	AA234935	ESTs	other
24058	2.0506511898	Z38211	Homo sapiens GDP-L-ascose pyrophosphorylase (GDPase) mRNA complete cds	other
30030	2.0505994824	AA481148	ESTs	other
61	2.0484705331	AC002115	Cytochrome c oxidase subunit Vb	?
6306	2.0474040935	X81625	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 EST - AA382517	?
8203	2.0473464771	AA382517	EST - AA382517	other
54357	2.0469305727	AA251430	ESTs Highly similar to RAS-RELATED PROTEIN RAS-10 [Canis familiaris]	other
36972	2.0468599712	AA442787	Tyrosine 3-monooxygenase/synaptophysin 5-monooxygenase activation protein beta polypeptide	?
28156	2.0459278063	AA489057	H.sapiens mRNA for nuclear protein SA-2	?
24434	2.045695222	V92787	ESTs	other
33508	2.0449481783	V68772	Human DNA sequence from cosmid F0811 on chromosome 5. Contains Daxx BING1 Tapasin RGL2 K22 BING4 BING5 ESTs and CpG islands	other
37681	2.0449346104	AA460075	H.sapiens mRNA for TRES	other
27125	2.0448658236	AA405505	Homo sapiens mRNA for putative RNA helicase 3' end	other
3780	2.0445300752	U09851	Zinc finger protein 148 (p12-82)	?
9112	2.0443252757	D16511	Coproporphyrinogen oxidase (coproporphyrinogen dehydratase)	TM
8357	2.044244223	AA418921	ESTs Highly similar to RSPS PROTEIN [Saccharomyces cerevisiae]	other
9133	2.0436113204	D30946	ESTs Highly similar to TRANSLOCATION-ASSOCIATED PROTEIN GAMMA SUBUNIT [Rattus norvegicus]	TM
7519	2.0414123824	AA147425	EST - AA147425_s	other
14701	2.0413755305	D59324	ESTs	other
380	2.0411495076	D28423	EST - D28423	?
20571	2.0346528604	N49585	ESTs	other
825	2.0329522889	D87328	Holo-carboxylase synthetase (biotin-(proprionyl)-Coenzyme A-carboxylase (ATP-hydrolyzing)) ligase	TM
27744	2.0318041265	AA452618	ESTs Weakly similar to HYPOTHETICAL PROTEIN H2034 [Haemophilus influenzae]	?
3987	2.0311206335	U19906	Arginine vasopressin receptor 1 (AVPR1)	?
22717	2.0302732387	R81394	EST - RC_R31394	?
377	2.0289078264	D28364	EST - D28364	other
28581	2.0274006552	C21163	EST	other
11790	2.0269672127	AA256678	ESTs Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]	other
27951	2.0269059272	AA478523	ESTs Weakly similar to IRI ALU SUBFAMILY J WARNING ENTRY IRI [H sapiens]	other
24678	2.0209181539	Z39349	ESTs Weakly similar to VACUOLAR ATP SYNTHASE 54 KD SUBUNIT [Saccharomyces cerevisiae]	other
10940	2.0209035614	AA122217	ESTs Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME II [C. elegans]	other
13964	2.0207518872	AA479048	ESTs	?
15665	2.019773566	V67831	Homo sapiens clone 24538 mRNA sequence	TM
28379	2.0189373185	AA009710	ESTs	other
13349	2.0172119305	AA449269	ESTs Weakly similar to MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR [Neurospora crassa]	SS
7322	2.0167797945	AA590652	ESTs Weakly similar to The KIAA0136 gene product is novel [H sapiens]	?
29358	2.0165298752	H70641	EST - RC_H70641	?

FIGURE 8 (cont.)

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24230	2.016017562	W72276	ESTs	other
42212	2.0158778169	H8535	Human clone 121711 defective manner transposon Humw2 mRNA sequence	?
729	2.01573779	D83778	Human mRNA for KIAA0194 gene partial cds	other
17951	2.0144787235	AA165526	Homo sapiens bifunctional ATP sulfurylase/adenosine 2-phosphosulfate kinase mRNA complete cds	other
33943	2.0135799277	AA171739	ESTs	other
5870	2.0118426199	X58244	Zinc finger protein 43 (HTF6)	other
36319	2.0116529739	AA425107	ESTs	other
25654	2.0097423819	AA126951	ESTs Weakly similar to DNA-directed RNA polymerase (D melanogaster)	other
16344	2.0090457727	AA018907	ESTs	?
8118	2.0090099575	AA328993	ESTs	other
29962	2.0087628098	N25228	ESTs	TM
32236	2.0078250796	R49327	Natural resistance-associated macrophage protein 2 PRECURSOR	TM
3279	2.0072427596	M94065	DEHYDROOROTATE DEHYDROGENASE PRECURSOR	TM
16255	2.0065069683	AA013349	ESTs	other
37872	2.0059209236	AA479215	EST - RC_AA479215	TM
41256	2.005858844	R31577	ESTs	other
34834	2.0050133743	AA290555	ESTs	other
23169	2.0039279023	T33215	ESTs	other
29851	2.0034762995	N22145	ESTs	other
32862	2	W32619	EST	?

FIGURE 8 (cont.)

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New Key Number	Accession	fold upregulated of Tumor over normal colon	Unigene Descriptor	
104860	AA007160	23	ESTs	SS
130016	AA055811	14	transmembrane glycoprotein	SS, TM
104954	AA074514	10	ESTs; Moderately similar to (define not available 4753765) [H.sapiens]	Other
105082	AA143763	7	ESTs; Weakly similar to Similarity to S. Pombe BEM1/BUD5 suppressor [C.elegans]	Other
109141	AA176428	7	ESTs	Other
108893	AA135894	6	retinoic acid induced 3	TM
108927	AA143493	5	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other
109027	AA157818	5	Human endogenous retroviral protease mRNA; complete cds	Other
133015	AA047036	4	ESTs	Other
114546	AA056263	4	ESTs; Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	Other
104974	AA085918	4	H.sapiens HUNK1 mRNA	Other
108695	AA121315	4	ESTs	SS
105049	AA132554	4	ESTs; Moderately similar to myosin heavy chain 12 [H.sapiens]	Other
133834	AA147510	4	Homo sapiens serine protease mRNA; complete cds	Other
109244	AA194237	4	ESTs; Weakly similar to C17H11.6 [C.elegans]	Other
128411	AA007555	3	ESTs; Weakly similar to transformation-related protein [H.sapiens]	SS, TM
114509	AA043551	3	ESTs	Other
104888	AA053660	3	ESTs	Other
114542	AA055768	3	ESTs	SS
132718	AA056731	3	Sjogren syndrome antigen A2 (60kD; ribonucleoprotein autoantigen SS-A/Ro)	Other
104953	AA074157	3	ESTs	Other
132784	AA099589	3	GDP dissociation inhibitor 2	Other
130962	AA102051	3	transmembrane 4 superfamily member 6	SS, TM
134421	AA122386	3	collagen; type V; alpha 2	SS
105035	AA128486	3	ESTs	Other
105039	AA130349	3	ESTs	Other
105062	AA134968	3	ESTs	Other
133817	AA148318	3	Human mRNA for KIAA0069 gene; partial cds	TM

FIGURE 9

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		ESTs; Highly similar to CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	
130335	AA156499	3: [H.sapiens]	Other
105132	AA159501	3: HBV associated factor	Other
109042	AA159525	3: ESTs	Other
109043	AA159605	3: ESTs	Other
132669	AA188378	ESTs; Weakly similar to 60S RIBOSOMAL 3: PROTEIN L22 [H.sapiens]	Other
135398	AA194075	3: nuclear receptor coactivator 4	Other
109344	AA213696	3: ESTs	SS
133221	AA235289	ESTs; Highly similar to rap2 gene product 3: [H.sapiens]	Other
114496	AA035611	ESTs; Weakly similar to !!! ALU SUBFAMILY SX WARNING ENTRY !!! 2: [H.sapiens]	Other
128635	AA043959	2: tropomyosin 4	Other
129912	AA047344	ESTs; Weakly similar to similar to WW/rsp5WWP domain containing proteins 2: [C.elegans]	Other
104927	AA058855	2: ESTs	SS
132821	AA070724	2: CD44 antigen (homing function and Indian blood group system)	Other
108409	AA075576	2: zm88h3.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:54545 3', mRNA sequence"	Other
133621	AA076138	2: H2A histone family; member Y	Other
108565	AA085342	2: ATPase; Ca++ transporting; cardiac muscle; slow twitch 2	TM
104977	AA088228	2: ESTs	Other
103777	AA093131	2: Homo sapiens PAC clone DJ0167F23 from 7p15	Other
108649	AA112540	2: ESTs	Other
114692	AA121995	2: ESTs; Weakly similar to Similar to potassium channel protein [C.elegans]	Other
105063	AA134985	2: ESTs	Other
133273	AA147725	2: dendritic cell protein	Other
128515	AA149044	ESTs; Highly similar to the KIAA0195 gene 2: is expressed ubiquitously [H.sapiens]	SS
105182	AA191014	2: ESTs; Weakly similar to Yd:372cp [S.cerevisiae]	Other
109277	AA196332	2: ESTs	Other
132608	AA199588	2: ARP3 (actin-related protein 3; yeast) homolog	Other
109380	AA219015	2: ESTs	Other
130800	AA223386	ESTs; Weakly similar to katanin p80 2: subunit [H.sapiens]	Other
129945	AA232104	ESTs; Highly similar to (define not 2: available 4929579) [H.sapiens]	Other
105305	AA233609	2: spindle pole body protein	Other

FIGURE 9
(Cont.)
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128924	AA234962	2. ESTs	TM
114895	AA236177	Homo sapiens mRNA for KIAA0887 protein; 2 partial cds	Other

FIGURE 9 (Cont.)

FIGURE 10
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A	B	C	D	E
1	1	1	1	1
2	2	2	2	2
3	3	3	3	3
4	4	4	4	4
5	5	5	5	5
6	6	6	6	6
7	7	7	7	7
8	8	8	8	8
9	9	9	9	9
10	10	10	10	10
11	11	11	11	11
12	12	12	12	12
13	13	13	13	13
14	14	14	14	14
15	15	15	15	15
16	16	16	16	16
17	17	17	17	17
18	18	18	18	18
19	19	19	19	19
20	20	20	20	20
21	21	21	21	21
22	22	22	22	22
23	23	23	23	23
24	24	24	24	24
25	25	25	25	25
26	26	26	26	26
27	27	27	27	27
28	28	28	28	28
29	29	29	29	29
30	30	30	30	30
31	31	31	31	31
32	32	32	32	32
33	33	33	33	33
34	34	34	34	34
35	35	35	35	35
36	36	36	36	36
37	37	37	37	37
38	38	38	38	38
39	39	39	39	39
40	40	40	40	40
41	41	41	41	41
42	42	42	42	42
43	43	43	43	43
44	44	44	44	44

FIGURE 10 (CONT)
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A	B	C	D	E
45	26004	AA24397	ESTs, Weakly similar to PEANUT PROTEIN [Diospyros melanocarpa]	other
46	27055	AA02642	ESTs	other
47	10844	AA100719	non-specific cross reacting antigen	other
48	11358	AA32104	ESTs	other
49	17389	AA121315	ESTs	other
50	17415	AA122386	Collagen, type XI, alpha 2	?
51	23772	T92735	ESTs	TM
52	25331	AA070947	Protophyasin 4	other
53	25354	AA081438	Histone macroH2A.1.2	SS TM
54	27039	AA081455	ESTs	other
55	27261	AA25344	Hemo sapiens clone 23699 mRNA, complete cds	other
56	27393	U89946	SFTS protein kinase 1	other
57	27413	U87213	collagen, type XI, alpha 1	SS
58	30015	U87213	stimulating growth factor beta-induced, 6kD	other
59	35519	X69700	collagen type III, alpha 1 (Ehlers-Danlos syndrome type IV; autosomal do	other
60	5562	X12876	varicella 1B	other
61	11818	AA251902	Hemo sapiens lymphoblastoid (LPL1) mRNA, complete cds	other
62	17666	AA147725	Hemo sapiens GA17 protein mRNA, complete cds	other
63	18024	AA184878	ESTs; Highly similar to 6S RIBOSOMAL PROTEIN L22 [Rattus norvegicus]	other
64	20841	N90933	ESTs	other
65	13612	AA458899	ESTs; Highly similar to [define not available 412715] [H.sapiens]	TM
66	17789	AA157818	Human endogenous retroviral protease mRNA, complete cds	other
67	25244	AA075182	Sjögren syndrome antigen A2 (SLD, ribonucleoprotein autoantigen SS-A/R	?
68	25583	AA131162	ESTs	other
69	27170	R67237	retroviral transition initiation factor 3, subunit 8 (48kD)	other
70	32198	Z33558	coatamer protein complex subunit alpha	SS
71	3351	AA33208	non-specific cross reacting antigen	SS
72	3551	AA33208	non-specific cross reacting antigen	other
73	8158	AA327530	Hemo sapiens GWI12 protein (GWI12) mRNA, complete cds	other
74	9207	D79652	Human polyA-binding protein processed pseudogene3	other
75	15051	U84681	ESTs; Moderately similar to III ALU SUBFAMILY SP WARMING ENTRY II	TM
76	15814	W63627	Hemo sapiens clone 23697 unknown mRNA, partial cds	other
77	25323	AA070485	ESTs; Highly similar to KIAA18 [H.sapiens]	TM
78	25323	AA070485	ESTs; Highly similar to KIAA18 [H.sapiens]	TM
79	25549	AA127058	ESTs; Weakly similar to predicted using Genefinder [C.aingens]	TM
80	25549	AA131165	heterogeneous nuclear ribonucleoprotein A2/B1	other
81	27464	AA441971	Hemo sapiens mRNA for KIAA454 protein, complete cds	TM
82	28212	R31190	ESTs	?
83	38037	AA488991	Hemo sapiens chaperonin containing 1-complex polypeptide 1, beta subunit	other
84	38457	AA038714	Lon protease-like protein	other
85	38457	AA038714	H.sapiens mRNA for 502p-like protein	other
86	37165	U83874	ribosomal RNA primase	other
87	6892	C90098	ESTs	other
88	12078	AA431181	ESTs	other

FIGURE 10 (CONT)
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A	B	C	D	E
89	17627	AA15884	Homo sapiens paralog 6 protein-coupled receptor (RANG6) Retinoid acid 1	TM
90	22952	N8921	ESTs; Weakly similar to nicotinic [H sapiens]	other
91	22954	T17185	ESTs	other
92	25808	AA18161	ESTs	other
93	27169	AA18479	proteasome (prosome, macropain) 26S subunit, non-ATPase 11	other
94	26096	AA48062	ESTs; Moderately similar to ubiquitous TPR motif Y isoform [H sapiens]	other
95	26706	DS4289	ESTs	other
96	35998	Z39041	ESTs; Weakly similar to DNA-DIRECTED RNA POLYMERASE III LARGE	TM
97	37863	AA45521	E2F transcription factor 5, p13-binding	other
98	38217	C18524	ESTs	SS TM
99	39217	D20002	HMG(S972) Human promyelocyte Homo sapiens cDNA clone pm2344 3'	other
100	2767	A03783	R2D histone family, member Z	other
101	5463	A03783	heterogeneous nuclear ribonucleoprotein A1	other
102	9243	A03783	heterogeneous nuclear ribonucleoprotein A1	other
103	14791	T39725	ESTs; Highly similar to 5-Semaphorin-4-carboxamide-beta-D-ribose	other
104	14804	148195	ESTs; Highly similar to 5-Semaphorin-4-carboxamide-beta-D-ribose	other
105	15974	AA07024	CD44 antigen (homing function and lectin-like)	other
106	20031	N21005	Homo sapiens androgen receptor associated protein A1 (BR-320) mRNA 9	TM
107	25484	AA12679	ESTs; Weakly similar to alternatively spliced product using exon 13A [H sa]	SS
108	26830	AA347559	lysylase (renal amyloidosis)	other
109	26968	AA490212	histone macropH2A1.2	other
110	30071	N33011	replication protein A3 (14kD)	other
111	32740	VO1600	von Hippel-Lindau syndrome	other
112	33870	AA416745	heterogeneous nuclear ribonucleoprotein A1	other
113	41853	T59161	Thymosin beta 1	TM
114	5011	X6401	proteasome (prosome, macropain) subunit beta type 5 [large multilocation]	?
115	5213	D65079	ESTs; Weakly similar to HADH-UBIQUINONE OXIDOREDUCTASE CHAI	other
116	8313	D78931	ESTs	TM
117	10985	R43963	ESTs; Highly similar to LEUCY-TRNA SYNTHETASE CYTOPLASMIC	other
118	12553	AA198501	ESTs; Highly similar to LEUCY-TRNA SYNTHETASE CYTOPLASMIC	other
119	11107	AA198501	ESTs; Highly similar to LEUCY-TRNA SYNTHETASE CYTOPLASMIC	other
120	11846	AA325869	ESTs; Highly similar to LEUCY-TRNA SYNTHETASE CYTOPLASMIC	other
121	12676	AA424348	ESTs; Weakly similar to myosin heavy chain 15 (197 12 box)	other
122	13772	AA454708	ESTs; Weakly similar to myosin heavy chain 15 (197 12 box)	SS
123	16728	AA033102	cadherin 17, LI cadherin (liver-intestine)	SS TM
124	17774	AA186243	cadherin 17, LI cadherin (liver-intestine)	other
125	21388	R20559	ESTs; Highly similar to (celline not available 412715) [H sapiens]	other
126	25433	AA095649	GDP dissociation inhibitor 2	TM
127	25603	AA120032	Homo sapiens CAH10a (CAH10) mRNA; partial cds	other
128	25791	AA199880	ELM, mat1 kinase	other
129	26163	AA326267	ESTs	?
130	26465	AA395527	ESTs; Weakly similar to TLS-associated protein TASH [H sapiens]	other
131	27122	AA186877	ESTs	other
132	25365	C14060	mat1, gamma 1	other

FIGURE 10 (CONT)
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A	B	C	D	E
133	28626	D25600	Human sapiens DNA from chromosomes 19, centromid R3B19 containing USF-2	other
134	28697	D51241	Human sapiens mRNA for putative vacuolar protein ATPase membrane act	SS, TM
135	28850	N04608	vesicular H(+)-ATPase subunit	other
136	33912	W41403	EST's; Moderately similar to neuronal thread protein ADT-NTP [H sapiens]	other
137	33912	W41403	EST's; Moderately similar to neuronal thread protein ADT-NTP [H sapiens]	other
138	40121	H04692	EST's; Highly similar to ribonucleoprotein G	other
139	40121	H04692	EST's; Highly similar to ribonucleoprotein G	other
140	40167	H06377	EST's; Moderately similar to putative G-binding protein [H sapiens]	other
141	446	D30773	colлагene, type XI, alpha 1	other
142	3530	D30773	colлагene, type XI, alpha 1	other
143	7835	AA32436	DIFFERENTIATION-DEPENDENT GENE 2	other
144	10988	AA32436	Human sapiens lysophospholipase (LPL) mRNA; complete cds	other
145	10985	AA121979	proteasome (prosome, macropain) subunit, beta type; 9 large multiclonal	other
146	11015	AA134138	EST's; Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]	other
147	11895	AA143783	EST's; Weakly similar to Similarity to S. Pombe BGLT1/BD5 suppressor [C	other
148	13388	AA279420	EST's; Highly similar to (define not available 433735) [H sapiens]	TM
149	15464	AA451676	EST's	other
150	17619	V029391	proliferation-associated 254, 384D	other
151	18225	AA138406	EST's	other
152	18225	AA138406	EST's	other
153	20500	N03927	EST's; Weakly similar to phenylethylamine binding protein [H sapiens]	7
154	20590	AA329151	EST's; Weakly similar to coded for cy C. elegans cDNA y1c1.3 [C. elegans]	other
155	27624	AA459112	Human sapiens mRNA for putative ribonucleoprotein G	other
156	27782	AA460358	EST's; Weakly similar to DNA-DIRECTED RNA POLYMERASE II H K2 P	other
157	28231	AA600153	DEK gene	other
158	28772	D59711	EST's	other
159	35363	N47556	eukaryotic translation initiation factor 3, subunit 3 (gamma, 41D)	other
160	35928	V047620	EST's; Weakly similar to reverse transcriptase related protein [H sapiens]	other
161	35655	H11320	Human sapiens HRHFB2115 mRNA; partial cds	TM
162	40175	H06605	peptidylglycyl isomerase B (cyclophilin B)	other
163	40886	N06691	EST's; Highly similar to (define not available 427914) [H sapiens]	other
164	40730	H04222	EST's; Weakly similar to 25 kDa trypsin inhibitor [H sapiens]	other
165	5318	U05105	poly(A)-binding protein-like 1	7
166	5318	U05105	poly(A)-binding protein-like 1	7
167	12342	AA459118	GRAVIN	other
168	13154	AA459118	Human sapiens liver mitochondrial membrane translocase Tim23 (TIM23)	other
169	14276	AA459118	Human sapiens liver mitochondrial membrane translocase Tim23 (TIM23)	other
170	15771	V05348	EST's	other
171	20588	N62345	Human sapiens Mdm1/TRA1b mRNA; complete cds	TM
172	24021	V042557	EST's	other
173	24250	V04712	calistatin	other
174	25245	AA057668	EST's	SS
175	25480	AA059429	SPlicing FACTOR U2AF 35 KD SUBUNIT	TM
176	25962	AA128904	heterogeneous nuclear ribonucleoprotein U (beta fold attachment factor A)	other

FIGURE 10 (CONT)
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A	B	C	D	E
177 28745	2,2	calcitonin 1		other
178 31957	2,2	tumor necrosis factor (TNF) 1		other
179 34481	2,2	human MD subunit 1 (MD1) (MD159) mRNA, complete cds		other
180 34481	2,2	MD159 mRNA, complete cds		other
181 37703	2,2	ESTs; Weakly similar to apolipoprotein III synthase, URQUIS [H sapiens]		TM
182 315	2,1	Human mRNA for KIAA2 gene, complete cds		TM
183 2449	2,1	M21259	small nuclear ribonucleoprotein polypeptide E	?
184 3326	2,1	M68458	ER LUMEN PROTEIN RETAINING RECEPTOR 2	TM
185 4197	2,1	U31556	EF2 transcription factor 5, p13-binding	other
186 481	2,1	U62862	eukaryotic translation initiation factor 3, subunit 6 (480D)	other
187 5417	2,1	X01060	transferrin receptor (tg, CD71)	TM
188 6334	2,1	X53228	cadherin 17; L1 cadherin (liver-intestine)	SS, TM
189 6625	2,1	X99133	NEUTROPHIL GELATINASE-ASSOCIATED UPOCAIN PRECURSOR	?
190 10471	2,1	A032442	ESTs; Highly similar to KERATIN, TYPE CYTOSKELETAL 14 Homo sa	other
191 11027	2,1	A114318	Human mRNA for KIAA9 gene, partial cds	TM
192 11116	2,1	A1181292	INTERFERON-ALPHA INDUCED T1.5 KD PROTEIN	other
193 11540	2,1	A030892	ESTs; Moderately similar to IIIA10 SUBFAMILY J WARNING ENTRY III	other
194 11837	2,1	A030895	ESTs; Weakly similar to Similarity 19 Yeast hypothetical protein YOR3160	other
195 12312	2,1	A111189	epidermal keratin-derived factor	other
196 12312	2,1	A111189	epidermal keratin-derived factor	other
197 20172	2,1	N25259	ESTs; Weakly similar to apolipoprotein III synthase, URQUIS [H sapiens]	other
198 20946	2,1	N51482	Human sapiens clone 528, unknown mRNA, complete sequence	other
199 20997	2,1	N51482	ESTs	other
200 27196	2,1	A4412452	ESTs	other
201 28026	2,1	A448433	ESTs; Weakly similar to deduced amino acid sequence in highly homologous	other
202 28187	2,1	A5321256	ESTs; Highly similar to nuclear pore complex protein NUPT [R. norvegicus]	other
203 28338	2,1	A621604	ESTs	other
204 28719	2,1	D59570	ESTs	other
205 28886	2,1	F04874	Homo sapiens mRNA for KIAA746 protein, partial cds	other
206 32124	2,1	R46008	eukaryotic translation initiation factor 3, subunit 7 (beta, 666P80)	other
207 33433	2,1	V050444	ESTs; Highly similar to (partial not available 4454324) [H sapiens]	other
208 33654	2,1	V050444	ESTs; Moderately similar to ganglioside-induced differentiation associated	other
209 33778	2,1	A4412270	ESTs	?
210 35588	2,1	A630151	calcitonin B	other
211 35588	2,1	D53131	epidermal keratin-derived factor	other
212 38545	2,1	H18323	ESTs; Weakly similar to similar to Yeast hypothetical protein LA182, 12 kDa	SS, TM
213 39977	2,1	H18323	Homo sapiens EF2-related transcription factor (EF2-R) mRNA, complete cds	other
214 40378	2,1	N27188	ESTs	other
215 41795	2,1	T26799	ESTs; Highly similar to TYROSINE-PROTEIN KINASE RECEPTOR EPH-	TM
216 1714	2	L09604	proteoglycan protein 2 (cosmic epithelium-enriched)	TM
217 201	2	L33930	Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region	TM
218 3278	2	M94556	single-stranded DNA-binding protein	other
219 4145	2	U28749	High-mobility group (nonhistone chromosomal) protein isoform 1-C	TM
220 8169	2	A4364267	ESTs; Highly similar to HYPOTHETICAL 63.7 KD PROTEIN Z0751.1 NC	other

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FIGURE 10 (CONT)
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A	B	C	D	E
221	9844	N3367	ESTs; Highly similar to NEDD-4 PROTEIN [Homo sapiens]	other
222	14032	AA46092	ESTs; Weakly similar to CH-TOG PROTEIN [H. sapiens]	TM
223	15395	AA05973	ESTs; Moderately similar to (define not available 418879) [H. sapiens]	TM
224	17827	AA112540	ESTs	TM
225	23033	T30481	ubiquitin-conjugating enzyme E2E 1 (homologous to yeast UBC4/5)	other
226	25525	AA13389	ESTs; Weakly similar to neuronal breast protein ADTC-NTP [H. sapiens]	other
227	26101	AA09494	ESTs	other
228	26700	AA11119	Neocortical protein S26	other
229	26965	H21119	Neurotrophin-inducible protein 2 (adipogen 2)	other
230	32181	RG7083	other	SS, TM
231	32897	MA5594	9-methylglutaryl (CD73)	other
232	10742	AD07480	ESTs; Weakly similar to HYPOTHETICAL 55, 50 PROTEIN IN CP32A1P	other
233	27195	AA46044	ESTs; Weakly similar to KIAA512 protein [H. sapiens]	other
234	28706	D5-296	Human mRNA for KIAA355, gene, complete cds	TM
235	35414	AA430186	ESTs	other
236	9979	N91007	ESTs; Weakly similar to F55A12.9 [C. elegans]	other
237	9807	N95507	ESTs; Weakly similar to KIAA319 [H. sapiens]	TM
238	10656	AA04790	ESTs	other
239	14877	U37546	apoptosis inhibitor 1	TM
240	27065	AA41094	Human mRNA for KIAA338, gene, complete cds	other
241	31913	H12948	Engrailed	SS
242	31913	N92339	ESTs	other
243	38272	AA11119	CD44	other
244	41386	R53423	CD44	other
245	41866	T87710	CD44	other
246	8439	AA435304	Homo sapiens androgen receptor associated protein 24 (AR24) mRNA, c	other
247	10311	AA001836	ESTs	other
248	10859	AA112149	ESTs	other
249	11279	AA213410	ESTs	SS
250	13548	AA450033	ESTs; Highly similar to HYPOTHETICAL 1,4 KD PROTEIN IN UBPP-SPT	other
251	14340	AA599653	Homo sapiens TOFL mRNA for transcription factor-like 5, complete cds	other
252	32180	RG3727	ESTs	other
253	35187	AA389722	ESTs	other
254	37254	AA452493	ESTs	TM
255	38144	RG4754475207	"Oncogene M-LAM, Fusion Activated"	other
256	40122	V01516	REACTIN, TYPE II CYTOSOLIC ETAL 60	SS, TM
257	16972	AA059822	Protein tyrosine kinase binding protein	other
258	23427	H170352	ESTs; Highly similar to PDL POLY(PT) PROTEIN [Sardinia sea bass virus]	other
259	25718	AA156941	protein with multiple spots versus near 10 focus on 4F8.3	other
260	33459	WR3403	ESTs; Weakly similar to cdt, hypothetical protein [E.coli]	other
261	36574	AA434454	ESTs	SS
262	41549	RG2846	trans- like growth factor 2 (transferrin A)	TM
263	2336	M17863	trans- like growth factor 2 (transferrin A)	other
264	6388	X63371	beta1 (band 1) [Drosophila] homolog 1	other

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FIGURE 10 (CONT)

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A	B	C	D	E
285	1.2	Z32203	ESTs	other
286	1.2	A411613	Human (alpha)	other
287	1.2	W01195	ESTs	other
288	1.2	A4347891	ESTs	other
289	1.2	A4100273	ESTs	other
290	1.2	A4135663	ESTs. Weakly similar to putative p15 [H.sapiens]	other
291	1.2	38477	ESTs	other
292	1.2	A459039	ESTs	other
293	1.2	R02547	ESTs	other
294	1.2	T51150	ESTs	other
295	1.2	A440047	Human sapiens mRNA for neuropilin, complete cds	other
296	1.1	M81549	SERUM AMYLOID A-4 PROTEIN PRECURSOR	SS
297	1.1	S81198	BPLP	other
298	1.1	X90579	H.sapiens DNA for cyp related pseudogene	?
299	1.1	N62889	ESTs	other
300	1.1	AJ004502	oreobrodes (P5-phosphoadenylyl-sulfate galactose/caramide 3') subtransfer	TM
301	1.1	H13849	ESTs	other
302	1.1	N14890	ESTs	TM
303	1.1	N19560	Human sapiens BmiL1 mRNA, complete cds	other
304	1.1	A41813	ESTs	other
305	1.1	A4461489	ESTs	other
306	1.1	A447866	ESTs	other
307	1.1	A4521342	ESTs	other
308	1.1	AA059018	ESTs	other
309	1.1	N23563	ESTs. Moderately similar to III ALU CLASS C WARNING ENTRY III [H.sapiens]	other
310	1.1	N40559	ESTs. Highly similar to LEUKOTOXIN SECRETION ATP-BINDING PROT	other
311	1.1	R41772	EST	other
312	1.1	R43540	ESTs	other
313	1.1	M93143	"Human sapiens plasminogen-like protein (PLGL) mRNA, complete cds"	other
314	1.1	X53085	Accesion not listed in Genbank	?
315	1.1	X95953	SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1	other
316	1.1	N43660	ESTs	other
317	1.1	N43660	Human sapiens mRNA for RGA49 protein, complete cds	other
318	1.1	N28947	ESTs. Highly similar to D103080P04 RNA SPlicing PROTEIN MS	other
319	1.1	N68725	metopon cultured protein kinase-activated protein kinase 2	other
320	1.1	AA233868	ESTs	TM
321	1.1	R41993	ESTs	TM
322	1.1	AA065081	"Zm13a.41 Stratiocarpus parviflorus (P33726) Homo sapiens cDNA clone IMA	other
323	1.1	H04086	ESTs. Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]	other
324	1.1	A4302772	ESTs. Weakly similar to neuronal breast protein AD7c-NTP [H.sapiens]	other
325	1.1	AA342526	ESTs. Moderately similar to unknown [H.sapiens]	other
326	1.1	AA400521	ESTs	other
327	1.1	AA468449	ESTs	other
328	1.1	C21330	ESTs	other
329	0.9	H04535-H14940	Denatrin	other

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FIGURE 10 (CONT)
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	A	B	C	D	E
309	5952	0.9	N94146	ESTs	other
310	10084	0.9	R32522	ESTs	other
311	11701	0.9	AA255546	ESTs	other
312	12083	0.9	AA207566	Human mRNA for KIAA187 gene, complete cds	other
313	15287	0.9	W13098	ESTs	other
314	15901	0.9	Z26905	Immunoglobulin superfamily, member 3	SS
315	21906	0.9	R43512	ESTs	other
316	22002	0.9	R43459	ESTs	other
317	24138	0.9	R43459	ESTs	other
318	24138	0.9	D45719	ESTs	other
319	26168	0.9	H60824	ESTs	other
320	32610	0.9	T81522	Human clone 2723 mRNA, partial cds	ESTM
321	33674	0.9	W02123	EST	other
322	35428	0.9	AA401409	ESTs	other
323	38504	0.9	AA556209	ESTs, Moderately similar to neuronal breast protein AD7c-NTP [H sapiens]	other
324	244	0.8	D14446	hemoglobin-like 1	TM
325	14304	0.8	AA460360	ESTs	other
326	25250	0.8	AA056210	ESTs	other
327	9971	0.7	N87590	ESTs	other
328	20461	0.7	N54429	ESTs	other
329	41028	0.7	R00815	homogentisate 1,2-dioxygenase (homogentisate oxidase)	other
330	41995	0.9	171012	hemogen, B beta polypeptide	ESTM

FIGURE 11
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
134804	12.3	L37036	small inducible cytokine subfamily B (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)	TM
130517	11.4	M90516	glutamine-fructose-6-phosphate transaminase 1	TM
104209	10.6	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated	SS
109991	10	H09613	ESTs	TM
124315	8.3	H94992	v-rat simian leukemia viral oncogene homolog A (ras related)	Other
132977	8.2	U28686	RNA binding motif protein 3	Other
130407	7.4	N29888	ESTs	Other
116176	6.6	AA463725	ESTs; Weakly similar to KIAA0226 [H.sapiens]	Other
119271	6.5	T16367	ESTs	Other
134711	6.5	X04011	cytochrome b-245; beta polypeptide (chronic granulomatous disease)	TM
134326	6.1	U16306	"Human chondroitin sulfate proteoglycan versican V splice-variant precursor peptide mRNA, complete cds"	Other
125852	5.9	H09290	ESTs; Weakly similar to unknown [H.sapiens]	SS, TM
112169	5.9	R48559	ESTs	TM
132528	5.9	AA283006	chromosome-associated polypeptide C	Other
134367	5.7	X54199	phosphoribosylglycinamide formyltransferase; phosphoribosylglycinamide synthetase; phosphoribosylaminimidazole synthetase	Other
111929	5.2	R40057	prominin (mouse)-like 1	SS, TM
102165	5	U18321	Death associated protein 3	Other
130441	5	U35835	protein kinase; DNA-activated; catalytic polypeptide	Other
133282	5	U52960	SRB7 (suppressor of RNA polymerase B; yeast) homolog	Other
100783	4.9	HG3748-H14 018	"Basic Transcription Factor, 44 Kda Subunit"	Other
122223	4.9	AA436158	ESTs	Other
104690	4.8	AA007160	ESTs	SS
113702	4.8	T97307	ESTs; Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	Other
101185	4.7	L19872	aryl hydrocarbon receptor	Other
105308	4.7	AA233744	ESTs	Other
107158	4.7	AA621540	ESTs	Other
101201	4.6	L22524	matrix metalloproteinase 7 (matrilysin; uterin)	SS
101809	4.5	M86849	"Homo sapiens connexin 26 (GJB2) mRNA, complete cds"	TM
101478	4.5	M23379	RAS p21 protein activator (GTPase activating protein) 1	Other
104695	4.5	AA012953	ESTs	Other
100365	4.4	D78611	mesoderm specific transcript (mouse) homolog	TM
126819	4.3	AA305536	"EST176522 Colon carcinoma (Caco-2) cell line H Homo sapiens cDNA 5' end, mRNA sequence"	Other
101890	4.3	M97925	defensin; alpha 5; Paneth cell-specific	SS
126838	4.2	AA858097	pigment epithelium-derived factor	Other
101684	4.2	M63256	cerebellar degeneration-related protein (22kD)	Other
117634	4.2	N36421	ESTs; Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	Other
132109	4.1	AA599801	ESTs	Other
115054	4.1	AA252863	ESTs	Other
106553	4	AA454967	ESTs	Other
119717	3.9	W69134	ESTs	Other

FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
131945	3.9	M67339	replication factor C (activator 1) 4 (37kD)	Other
128790	3.9	AA291725	secreted frizzled-related protein 4	SS
120562	3.8	AA280036	ESTs; Weakly similar to W01A6.c [C.elegans]	SS
105517	3.7	D60799	ESTs	Other
102618	3.7	U85932	extracellular matrix protein 1	SS
106286	3.7	AA344441	frizzled (Drosophila) homolog 7	Other
133640	3.6	D63004	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Other
100335	3.6	D63391	platelet-activating factor acetylhydrolase; isoform Ib; gamma subunit (29kD)	Other
104720	3.6	AA018441	ESTs	Other
107348	3.6	U43701	ribosomal protein L23a	Other
134969	3.6	AA236324	ESTs; Weakly similar to !!!!! ALU CLASS A WARNING ENTRY !!!!! [H.sapiens]	SS
111345	3.6	N89820	ESTs	Other
107053	3.6	AA600147	ESTs; Weakly similar to Similar to NADH-cytochrome B5 reductase [C.elegans]	Other
107240	3.5	D59366	ESTs	Other
107129	3.5	AA620553	flap structure-specific endonuclease 1	Other
134646	3.5	AA431505	Homo sapiens mRNA for putative Sqv-7-like protein; partial	TM
101897	3.5	S58544	sperm associated antigen 1	Other
107151	3.5	AA621169	ESTs	Other
108012	3.4	AA411621	ESTs	Other
101950	3.4	S79211	propionyl Coenzyme A carboxylase; alpha polypeptide	Other
116844	3.4	H64938	ESTs	Other
128025	3.4	AA937173	ESTs	TM
106785	3.4	AA478587	leukemia associated gene 1; candidate tumor suppressor frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	Other
104518	3.4	R09615	proteasome (prosome; macropain) 26S subunit; ATPase; 5	Other
117897	3.4	N39214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase	Other
104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) [H.sapiens]	Other
105372	3.3	AA236461	ESTs	Other
104896	3.3	AA054226	ESTs	Other
113485	3.3	T87863	ESTs	Other
127003	3.3	AA550806	ESTs; Weakly similar to (define not available 3582151) [H.sapiens]	TM
100305	3.3	D50467	DEAD/H (Asp-Glu-Ala-Asp/Hfs) box polypeptide 8 (RNA helicase)	SS
134722	3.2	W47183	ESTs; Weakly similar to !!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!! [H.sapiens]	Other
126801	3.2	AA512902	ESTs	SS, TM
133503	3.2	M33195	Fc fragment of IgE; high affinity I: receptor for; gamma polypeptide	SS, TM
132183	3.2	L19183	Human MAC30 mRNA; 3' end	TM
105298	3.2	AA233459	ESTs	TM
111046	3.2	N55514	ESTs; Moderately similar to !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! [H.sapiens]	TM
135309	3.2	D25084	ESTs	SS
102808	3.2	U90426	nuclear RNA helicase; DEAD variant of DEAD box family	Other
100552	3.1	HG2167-H72 237	"Protein Kinase H131, Camp-Dependent"	Other
127652	3.1	AA804487	ESTs	Other

FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
116127	3.1	AA459703	ESTs; Moderately similar to coded for by <i>C. elegans</i> cDNA CEESD54F [<i>C. elegans</i>]	TM
131904	3.1	AA143019	ESTs; Highly similar to surface 4 integral membrane protein [<i>H.sapiens</i>]	TM
126547	3.1	U47732	transmembrane 4 superfamily member 3	Other
102823	3.1	U90914	carboxypeptidase D	SS
132268	3.1	N41849	Homo sapiens cytokine receptor related protein 4 (CYTOR4) mRNA; complete cds	Other
127445	3.1	AA905286	ESTs	Other
134395	3.1	L09717	lysosomal-associated membrane protein 2	SS, TM
105743	3.1	AA293300	ESTs; Weakly similar to semaphorin C [<i>M.musculus</i>]	Other
125827	3.1	AI471525	YY1 transcription factor	Other
101229	3.1	L27943	cytidine deaminase	Other
102306	3	U33317	defensin; alpha 5; Paneth cell-specific	SS
107318	3	T74445	"yc82f6.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:2242 5', mRNA sequence"	Other
120983	3	AA398208	EST	Other
134700	3	AA481414	golgi SNAP receptor complex member 1	TM
131216	3	D31058	ESTs	SS
127565	3	D79516	"HUM272B04B Human aorta polyA+ (TFujiiwara) Homo sapiens cDNA clone GEN-272B04 5', mRNA sequence."	Other
106802	2.9	AA469209	ESTs	Other
130874	2.9	T08287	ESTs	Other
101275	2.9	L37539	Ts translation elongation factor; mitochondrial	Other
111179	2.9	N67239	ESTs	Other
126086	2.9	H70975	"yr73g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210960 5', mRNA sequence."	Other
105365	2.9	AA236275	ESTs	Other
118789	2.9	N75416	ESTs	Other
115117	2.9	AA256492	<i>H.sapiens</i> PAP mRNA	Other
100484	2.9	HG1103-HT1103	"Guanine Nucleotide-Binding Protein Rat, Ras-Oncogene Related"	Other
101300	2.9	L40391	Homo sapiens (clone s153) mRNA fragment	Other
103075	2.9	X59543	ribonucleotide reductase M1 polypeptide	Other
132164	2.8	UA4573	procollagen-lysine; 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2	Other
106716	2.8	AA464962	ESTs	Other
134098	2.8	X06323	Human MRL3 mRNA for ribosomal protein L3 homologue (MRL3	Other
134485	2.8	X92153	cathepsin K (pseudocystinosis)	SS
129634	2.8	AA150726	ESTs	Other
112207	2.8	R49602	ESTs	Other
124904	2.8	R68970	ESTs	Other
125471	2.8	AA477571	UDP-glucose ceramide glucosyltransferase	SS
132180	2.8	AA405569	fibroblast activation protein; alpha	SS
104454	2.8	M84443	galactokinase 2	TM
134282	2.8	T25508	ESTs	Other
101558	2.8	M32011	neutrophil cytosolic factor 2 (85kD; chronic granulomatous disease; autosomal 2)	Other
130529	2.8	AA173238	small inducible cytokine A5 (RANTES)	Other
101804	2.7	M86699	TTK protein kinase	Other

FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
109565	2.7	F01930	ESTs	Other
112427	2.7	R62604	ESTs	Other
115198	2.7	AA261819	ESTs	Other
121831	2.7	AA425374	ESTs	Other
132454	2.7	W78726	ESTs; Highly similar to serine/threonine kinase [H.sapiens]	Other
116399	2.7	AA599729	Homo sapiens homeobox protein A10 (HOXA10) gene; complete cds	Other
100409	2.7	D8957	Human mRNA for KIAA0202 gene; partial cds	Other
130987	2.7	R45698	ESTs	Other
107217	2.7	D51095	ESTs	SS, TM
125698	2.6	AA748483	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene; partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes; complete cds	SS
118722	2.6	N73563	ESTs	SS
104521	2.6	R11604	"y47c1.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:132 5, mRNA sequence"	Other
130800	2.6	AA223386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]	Other
134415	2.6	AA329274	protein tyrosine phosphatase type IVA; member 2	TM
118461	2.6	AA621557	ESTs; Moderately similar to I111 ALU SUBFAMILY SQ WARNING ENTRY I111 [H.sapiens]	Other
100854	2.6	HQ4297-HT4 567	Transcriptional Coactivator Pco4	Other
103818	2.6	AA150614	"z43h5.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:54729 5, mRNA sequence"	Other
105713	2.6	AA291321	ESTs	Other
114969	2.6	AA250775	ESTs	Other
130415	2.6	X07290	Human HF.12 gene mRNA	Other
101781	2.6	M83822	Human beige-like protein (BGL) mRNA; partial cds	Other
128131	2.6	A1283162	claudin 3	SS, TM
131564	2.6	AA491465	ESTs	Other
100279	2.6	D42084	Human mRNA for KIAA0094 gene; partial cds	Other
130149	2.6	J04031	methylentetrahydrofolate dehydrogenase (NADP+ dependent); methylenetetrahydrofolate cyclohydrolase; formyltetrahydrofolate synthetase	Other
119888	2.6	W81710	ESTs	SS
126638	2.6	AA649257	ESTs	Other
131672	2.6	X12901	Human mRNA for villin	Other
134405	2.6	J04177	collagen; type XI; alpha 1	Other
101188	2.5	L20320	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	TM
104534	2.5	R22303	ESTs; Weakly similar to putative p150 [H.sapiens]	Other
135179	2.5	U43747	Friedreich ataxia	SS
124308	2.5	H93575	ESTs	SS
125921	2.5	A051602	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	TM
101342	2.5	L76191	Interleukin-1 receptor-associated kinase 1	Other
129351	2.5	AA167268	ESTs	Other
103774	2.5	AA092998	ESTs; Weakly similar to R07G3.8 [C.elegans]	Other
131289	2.5	AA485697	ESTs	SS, TM
132094	2.5	W01996	ESTs; Highly similar to (define not available 4929683) [H.sapiens]	Other
103223	2.5	X74801	chaperonin containing TCP1; subunit 3 (gamma)	Other

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105610	2.5	AA279991	ESTs	Other
115719	2.5	AA416997	ESTs	Other
134888	2.5	AA148094	Tat-interacting protein (30kD)	Other
105564	2.5	AA262943	ESTs	Other
129689	2.5	AA130156	ESTs	Other
103391	2.5	X94453	pyroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	Other
104182	2.5	AA479990	ESTs; Weakly similar to glioma amplified on chromosome 1 protein [H.sapiens]	SS, TM
123494	2.5	AA599786	ESTs	Other
122905	2.5	AA470070	ESTs	Other
109175	2.5	AA180496	ESTs	Other
129907	2.5	D80170	ESTs	Other
115142	2.4	AA258116	ESTs; Weakly similar to !III ALU SUBFAMILY SQ WARNING ENTRY !III [H.sapiens]	Other
125474	2.4	AA151216	Homo sapiens 14-3-3 protein mRNA; complete cds	SS
125745	2.4	A1283493	ribophorin II	Other
100103	2.4	AF007875	dolichyl-phosphate mannosyltransferase polypeptide 1; catalytic subunit	Other
102887	2.4	U73379	Human cyclin-selective ubiquitin carrier protein mRNA; complete cds	Other
133710	2.4	U21049	epithelial protein up-regulated in carcinoma	SS, TM
109141	2.4	AA178428	ESTs	Other
132811	2.4	U25435	transcriptional repressor	Other
102862	2.4	X01057	Interleukin 2 receptor; alpha	SS, TM
104300	2.4	D37933	syntaxin 18	Other
105091	2.4	AA148859	ESTs; Moderately similar to !III ALU SUBFAMILY J WARNING ENTRY !III [H.sapiens]	Other
110674	2.4	H89315	*yw25e09.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253288 3', mRNA sequence.*	TM
122571	2.4	AA452600	EST	Other
123421	2.4	AA568440	ESTs; Moderately similar to neuronal thread protein AD7c-NTP [H.sapiens]	Other
132181	2.4	AA046939	ESTs; Moderately similar to !III ALU SUBFAMILY SX WARNING ENTRY !III [H.sapiens]	Other
129445	2.4	AA306121	ESTs	SS
113523	2.4	W80763	ESTs; Moderately similar to FK506-binding protein 65kD [M.musculus]	Other
100598	2.4	HG2483-HT2 559	Guanine Nucleotide-Binding Protein G25k	Other
130869	2.4	AA128100	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)	Other
132393	2.4	W58888	ESTs; Moderately similar to !III ALU SUBFAMILY SQ WARNING ENTRY !III [H.sapiens]	Other
100830	2.4	HG4074-HT4 344	Rad2	Other
133795	2.4	D21255	cadherin 11 (OB-cadherin; osteoblast)	SS, TM
100867	2.4	HG4315-HT4 586	Transketolase-Like Protein	Other
119859	2.4	W80702	ESTs	Other
135269	2.4	M77698	YY1 transcription factor	Other
115140	2.4	AA259030	ESTs; Weakly similar to (define not available 3874821) [C.elegans]	Other
102162	2.4	U18291	CDC16 (cell division cycle 16; S. cerevisiae; homolog)	Other

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FIGURE 11 (CONT)
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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
100372	2.4	D79997	KIAA0175 gene product	TM
106981	2.4	AA521157	ESTs	Other
130114	2.4	AA234717	ESTs	Other
116129	2.3	AA459996	ESTs	Other
122235	2.3	AA438475	ESTs	Other
107315	2.3	T62771	Homo sapiens nucleotides 3 (NPM3) mRNA; complete cds	SS
125905	2.3	T69968	chaperonin containing TCP1; subunit 2 (beta)	Other
133061	2.3	AB000584	prostate differentiation factor	SS
107531	2.3	Y13936	protein phosphatase 1G (formerly 2C); magnesium-dependent; gamma isoform	Other
125820	2.3	AA730136	teratocarcinoma-derived growth factor 1	Other
131725	2.3	AA456254	ESTs; Highly similar to (define not available 4176448) [H.sapiens]	Other
101228	2.3	L27706	chaperonin containing TCP1; subunit 5A (zeta 1)	Other
132571	2.3	R84594	ESTs; Highly similar to (define not available 4809026) [H.sapiens]	SS, TM
100090	2.3	AC002406	"Human BAC clone RG367017 from 7p15-p21, complete sequence [Homo sapiens]"	Other
103658	2.3	Z74615	collagen; type I; alpha 1	SS, TM
104807	2.3	AA054641	ESTs	Other
106818	2.3	AA480890	ESTs	Other
113077	2.3	T40442	ESTs	SS
128773	2.3	M28879	granzyme B (granzyme 2; cytotoxic T-lymphocyte-associated serine esterase 1)	SS
129506	2.3	AA258296	Homo sapiens mRNA for KIAA0877 protein; partial cds	TM
133746	2.3	U44378	MAD (mothers against decapentaplegic; Drosophila) homolog 4	Other
134272	2.3	X76040	Lon protease-like protein	Other
106267	2.3	AA431873	Homo sapiens clone 24711 mRNA sequence	Other
133493	2.3	AA284143	Homo sapiens chromosome 1 atrophin-1 related protein (ORPLA) mRNA; complete cds	Other
104278	2.3	C02582	ESTs; Highly similar to (define not available 5114045) [H.sapiens]	Other
127211	2.3	AA480935	"aa2bc03.r1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814564 5' mRNA sequence."	Other
110721	2.3	H97678	ESTs	Other
114774	2.3	AA150043	ESTs	TM
132968	2.3	N77151	Homo sapiens mRNA for KIAA0799 protein; partial cds	Other
106916	2.3	AA490814	ESTs	Other
113849	2.3	W60439	ESTs; Moderately similar to cbp146 [M.musculus]	Other
131028	2.3	U20240	CCAAT/enhancer binding protein (C/EBP); gamma	Other
130380	2.3	U56853	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130) mRNA; complete cds	SS
125390	2.3	H95094	KIAA0016 gene product	SS, TM
127256	2.3	AA327550	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
132116	2.3	AA234767	ESTs	SS, TM
117765	2.3	N47797	ESTs	Other
119126	2.3	R45175	ESTs	Other
129482	2.2	AA435849	ESTs; Moderately similar to unknown protein [H.sapiens]	Other
120493	2.2	AA255633	ESTs	SS
108927	2.2	AA143493	ESTs; Weakly similar to PLECKSTRIN [H.sapiens]	Other

FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated In Tumors	Exemplar Accession	Complete Title	ORF Structural Info
122520	2.2	AA449427	ESTs; Moderately similar to pregnancy-specific beta-1 glycoprotein 2 [H.sapiens]	Other
125982	2.2	R98091	RAE1 (RNA export 1; S.pombe) homolog	Other
132325	2.2	N37065	ESTs; Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
100287	2.2	D43950	Human mRNA for KIAA0098 gene; partial cds	Other
114895	2.2	AA236177	Human sapiens mRNA for KIAA0887 protein; partial cds	Other
105038	2.2	AA130273	ESTs; Weakly similar to (define not available 4240269) [H.sapiens]	Other
105476	2.2	AA255473	ESTs	SS
108942	2.2	AA496347	ESTs; Highly similar to gene 7442 protein [H.sapiens]	Other
110586	2.2	H59990	ESTs	Other
111068	2.2	N58397	ESTs	Other
127963	2.2	A1299013	*gn13h12.x1 NCL CGAP Lu5 Homo sapiens cDNA clone IMAGE:1898183 3' similar to TR:022813 022813 PUTATIVE NAD(P)-DEPENDENT "CHOLESTEROL DEHYDROGENASE", mRNA sequence.*	TM
130985	2.2	AA243700	ESTs	Other
132877	2.2	R40685	Human sapiens mRNA for KIAA0851 protein; complete cds	TM
135242	2.2	M74093	cyto E1	TM
129468	2.2	J03040	secreted protein; acidic; cysteine-rich (osteonectin)	SS
132816	2.2	AA386284	ESTs	SS, TM
133780	2.2	M14219	decorin	Other
121853	2.2	AA425887	ESTs	Other
114608	2.2	AA079381	ESTs	Other
129017	2.2	H13108	ESTs	SS
132725	2.2	L41887	splicing factor; arginine/serine-rich 7 (35kD)	Other
125606	2.2	R28463	ESTs	SS
105538	2.2	AA258860	ESTs; Highly similar to (define not available 4583654) [H.sapiens]	Other
133221	2.2	AA235289	ESTs; Highly similar to rap2 gene product [H.sapiens]	Other
106389	2.2	AA445949	ESTs	Other
128940	2.2	AA190993	a disintegrin and metalloproteinase domain 12 (metrin alpha)	Other
120969	2.2	AA398116	ESTs	Other
102495	2.2	U51240	Human mRNA for KIAA0085 gene; partial cds	TM
101124	2.2	L10343	protease inhibitor 3; skin-derived (SKALP)	SS
102778	2.2	U83463	syndecan binding protein (synterin)	Other
107307	2.2	T52099	creatine kinase; mitochondrial 2 (sarcomeric)	Other
111605	2.2	R11638	ESTs	Other
101959	2.2	S80343	arginyl-tRNA synthetase	Other
101031	2.2	J05070	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase; 92kD type IV collagenase)	SS
131701	2.2	AA149008	ESTs; Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII [H.sapiens]	Other
105344	2.2	AA235303	ESTs	TM
103166	2.2	X67951	proliferation-associated gene A (natural killer-enhancing factor A)	Other
131463	2.2	X74142	forkhead (Drosophila)-like 1	Other
131412	2.2	U34044	Human selenium donor protein (selD) mRNA; complete cds	Other
134982	2.2	N46086	ESTs	Other
127236	2.1	A1341818	budding uninhibited by benzimidazoles 1 (yeast homolog)	Other
104459	2.1	M91493	EST	Other

FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
124596	2.1	N70086	ESTs	Other
105650	2.1	AA282347	ESTs; Highly similar to (define not available 4454694) [H.sapiens]	Other
134917	2.1	X87241	FAT tumor suppressor (Drosophila) homolog	SS
132478	2.1	H20906	Homo sapiens mRNA for KIAA0746 protein; partial cds	SS, TM
134464	2.1	N79354	ESTs; Weakly similar to Rga [D.melanogaster]	Other
111221	2.1	N68669	ESTs	Other
100892	2.1	HG4557-HT4	962	Other
117170	2.1	H96153	ESTs	Other
124049	2.1	F10523	primase; polypeptide 2A (58kD)	Other
131992	2.1	D50914	Human mRNA for KIAA0124 gene; partial cds	TM
103003	2.1	X52003	'trefol factor 1 (breast cancer; estrogen-inducible sequence expressed in)	SS
134085	2.1	U20979	chromatin assembly factor I (150 kDa)	Other
126216	2.1	N23870	ESTs	Other
102721	2.1	U79241	Human clone 23759 mRNA; partial cds	Other
128040	2.1	AA918528	ESTs	Other
101038	2.1	J05249	replication protein A2 (32kD)	SS
106060	2.1	AA417287	C-terminal binding protein 2	Other
103822	2.1	Z48042	basic transcription factor 3	Other
127684	2.1	AA786630	ESTs	Other
130911	2.1	W72906	HIRA interacting protein 4 (dnaJ-like)	Other
104260	2.1	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA; complete cds	Other
120714	2.1	AA292689	ESTs	Other
101576	2.1	M34423	galactosidase; beta 1	SS
113443	2.1	T86158	ESTs	SS
101516	2.1	M28249	Accession not listed in Genbank	Other
105480	2.1	AA450373	ESTs; Moderately similar to [!!!!] ALU SUBFAMILY SB WARNING ENTRY [!!!!] [H.sapiens]	Other
111385	2.1	N92659	ESTs	Other
121121	2.1	AA399371	ESTs; Weakly similar to (define not available 4686925) [H.sapiens]	Other
124768	2.1	R40177	ESTs	Other
102501	2.1	U51566	Human shah binding protein 1 (ShahBP1) mRNA; partial cds	Other
106432	2.1	AA448650	ESTs	Other
132812	2.1	R48108	ESTs	Other
125681	2.1	AA394176	accessory proteins BAP3/BAP29	TM
130511	2.1	L32137	cartilage oligomeric matrix protein	Other
126219	2.1	AA978333	ESTs	Other
130962	2.1	AA102051	transmembrane 4 superfamily member 6	SS, TM
101840	2.1	M93056	protease inhibitor 2 (anti-elastase); monocyte/neutrophil	TM
123928	2.1	AA621363	EST	Other
132073	2.1	N67406	ESTs; Moderately similar to [!!!!] ALU SUBFAMILY SC WARNING ENTRY [!!!!] [H.sapiens]	Other
101671	2.1	M61832	S-adenosylhomocysteine hydrolase	Other
107059	2.1	AA008545	ESTs	Other
132791	2.1	AA446086	ESTs; Weakly similar to YY1-associated factor 2 [H.sapiens]	Other
103131	2.1	X55614	S100 calcium-binding protein P	Other
104791	2.1	AA029046	ESTs	Other

FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
135181	2.1	AA621349	ESTs; Weakly similar to similar to Yeast hypothetical protein L8167.12 like [C.elegans]	Other
104334	2.1	D82614	ESTs	Other
132103	2.1	AA025086	ESTs	Other
126743	2.1	AA179253	poly(A)-binding protein-like 1	Other
100430	2.1	D87453	Human mRNA for KIAA0264 gene; partial cds	Other
114860	2.1	AA235112	ESTs; Moderately similar to similar to murine RNA-binding protein [H.sapiens]	Other
116732	2.1	F13779	ESTs; Weakly similar to !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! [H.sapiens]	Other
131045	2.1	H30863	ESTs; Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canal protein. [H.sapiens]	Other
133209	2.1	AA1114183	ESTs; Moderately similar to glutamate pyruvate transaminase [H.sapiens]	Other
101758	2.1	M77836	Human pyroline 5-carboxylate reductase mRNA; complete cds	Other
102214	2.1	U23752	SRY (sex-determining region Y)-box 11	Other
130100	2.1	AA425593	ESTs	Other
109799	2.1	F10770	Homo sapiens clone 669 unknown mRNA; complete sequence	Other
130850	2.1	U69061	T-cell receptor; beta cluster	SS, TM
106885	2.1	AA461551	ESTs; Highly similar to 73 kDa subunit of cleavage and polyadenylation specificity factor [H.sapiens]	TM
125724	2.1	AA083407	stimulated trans-acting factor (80 kDa)	Other
134258	2.1	L28010	heterogeneous nuclear ribonucleoprotein F	Other
129642	2.1	R50008	7-dehydrocholesterol reductase	TM
125338	2.1	T86823	ESTs	Other
125303	2	Z39821	ESTs	Other
100749	2	HG3521-HT3 715	Ras-Related Protein Rap1b	Other
128185	2	AI39398	ESTs	TM
126880	2	AI151406	ESTs	SS, TM
105263	2	AA227926	ESTs	Other
123288	2	AA495836	EST	Other
105807	2	AA393803	ESTs	Other
105040	2	AA131047	KIAA0698 gene product	TM
131977	2	F09788	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase); alpha polypeptide II	SS
117992	2	N52000	ESTs	SS, TM
134037	2	X53586	Human mRNA for integrin alpha 6	SS
132744	2	X54326	glutaryl-prolyl-IRNA synthetase	Other
101581	2	M34996	"Human MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end"	SS, TM
103576	2	Z26317	desmoglein 2	SS
131235	2	AA223284	ESTs; Moderately similar to (define not available 4680395) [H.sapiens]	Other
127910	2	AA781881	ESTs; Weakly similar to sperm fertilization protein sp56 precursor [M.musculus]	SS
101552	2	M31642	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	Other
106318	2	AA438570	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	Other
101192	2	L20859	Human leukemia virus receptor 1 (GLVR1) mRNA; complete cds	TM
104592	2	R81003	Homo sapiens serine protease mRNA; complete cds	SS
129095	2	L12350	thrombospondin 2	SS

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FIGURE 11 (CONT)

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PRIMEKEY	Fold Upregulated in Tumors	Exemplar Accession	Complete Title	ORF Structural Info
105705	2	AA290767	ESTs	Other
128461	2	M63262	arachidonate 5-lipoxygenase-activating protein	SS, TM

Accession	Score	Source	Gene	Product
16074	>10	AA001507	ESTs	other
25047	>10	AA011031	ESTs	other
25082	>10	AA017257	ESTs	other
16490	>10	AA026418	ESTs	other
25179	>10	AA031298	H.sapiens mR	other
25215	>10	AA035540	APOLIPOPRO	other
25262	>10	AA044825	ESTs	other
16810	>10	AA053636	ESTs	other
16835	>10	AA054438	ESTs	SS,
10747	>10	AA055841	ESTs	other
10748	>10	AA055892	ESTs	other
16993	>10	AA065300	Human mRNA	other
17051	>10	AA070801	ESTs	TM
10840	>10	AA084104	ESTs	other
7295	>10	AA085661	ESTs	other
7325	>10	AA090842	ESTs Weakly	other
17419	>10	AA113349	EST	?
17541	>10	AA127459	ESTs	other
17559	>10	AA128407	ESTs	other
25689	>10	AA128978	ESTs	?
17800	>10	AA130596	ESTs	other
10992	>10	AA132523	Homo sapiens	other
17654	>10	AA133250	ESTs	TM
17734	>10	AA137246	ESTs	other
25801	>10	AA148530	EST - RC_AA	TM
25806	>10	AA149007	EST	?
11121	>10	AA156359	Human TAR O	?
11160	>10	AA164289	ESTs	other
25925	>10	AA164494	ESTs Weakly	other
25934	>10	AA165355	Human clone	?
17987	>10	AA169379	ESTs	other
18008	>10	AA171895	Homo sapiens	TM
33953	>10	AA173290	Human HOXA	other
33980	>10	AA180223	CAMP-DEPEN	other
34013	>10	AA190888	EST - RC_AA	other
34014	>10	AA191348	ESTs	other
34015	>10	AA191353	ESTs	TM
34070	>10	AA196549	ESTs	other
18260	>10	AA206801	ESTs	?
34105	>10	AA207123	ESTs	SS,
34107	>10	AA209469	ESTs	other
18330	>10	AA216722	Human mRNA	TM
18362	>10	AA223912	Ribonuclease	other
18392	>10	AA227751	ESTs	SS,
34188	>10	AA228030	ESTs	TM
34197	>10	AA232315	Homo sapiens	other
25948	>10	AA234365	Homo sapiens	?
25951	>10	AA234556	EST	?
11561	>10	AA236533	Evi-1	other
26059	>10	AA236685	ESTs	other
26100	>10	AA242835	Human mRNA	other
11603	>10	AA243052	ESTs Highly	other
7785	>10	AA243375	EST - AA2433	other
34372	>10	AA251973	ESTs	?
26240	>10	AA252282	Human mRNA	TM

FIGURE 12

34382	>10	AA252512	ESTs	other
34391	>10	AA252703	EST - RC_AA	other
26274	>10	AA253011	ESTs	?
34400	>10	AA253400	ESTs	other
26291	>10	AA253422	ESTs	?
26355	>10	AA256379	ESTs	other
11813	>10	AA258158	ESTs	other
34518	>10	AA278721	ESTs	?
28545	>10	AA278979	ESTs	other
28574	>10	AA279504	ESTs	other
34554	>10	AA280016	DNA polymerase	other
34561	>10	AA280298	ESTs	TM
26628	>10	AA280641	ESTs Highly	TM
11969	>10	AA280670	ESTs	SS,
34575	>10	AA280738	ESTs	TM
26677	>10	AA281636	ESTs	?
26700	>10	AA282197	EST	?
34672	>10	AA284372	ESTs	other
34682	>10	AA285079	ESTs	other
12143	>10	AA290991	ESTs	other
8092	>10	AA316272	ESTs	TM
34904	>10	AA321746	EST	other
8111	>10	AA323787	ESTs	other
8125	>10	AA330771	Human protein	TM
26916	>10	AA331393	ESTs	other
26926	>10	AA342402	ESTs	other
26935	>10	AA347193	ESTs Weakly	TM
35038	>10	AA350541	ESTs Moderate	TM
35049	>10	AA350857	ESTs	other
35106	>10	AA371561	EST Weakly	?
35197	>10	AA398120	ESTs	other
35277	>10	AA398536	ESTs	other
35309	>10	AA398660	EST	other
35322	>10	AA398710	H. sapiens RNA	TM
27037	>10	AA400198	ESTs	TM
35495	>10	AA400527	ESTs	?
27046	>10	AA400670	Homo sapiens	other
35500	>10	AA400715	ESTs	other
12480	>10	AA403116	Homo sapiens	other
35693	>10	AA405485	ESTs Weakly	other
35697	>10	AA405512	ESTs	other
35766	>10	AA405169	Homo sapiens	other
35769	>10	AA406206	ESTs	other
35798	>10	AA410231	ESTs	other
35801	>10	AA410291	ESTs	other
35803	>10	AA410295	ESTs	other
35822	>10	AA411144	ESTs	TM
35874	>10	AA412024	EST	?
35956	>10	AA412560	ESTs	other
36052	>10	AA417027	EST	TM
36258	>10	AA423962	ESTs Weakly	other
36288	>10	AA424502	ESTs	other
36307	>10	AA424803	EST	?
36371	>10	AA426017	ESTs	TM
36395	>10	AA426353	ESTs	other
36405	>10	AA426406	Homo sapiens	other

FIGURE 12
(cont.)

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36506	>10	AA429610	ESTs	other
36571	>10	AA430726	EST - RC_AA	SS,
36695	>10	AA433910	ESTs	other
36739	>10	AA435610	EST - RC_AA	?
36753	>10	AA435686	ESTs	other
36845	>10	AA436198	ESTs	?
13136	>10	AA436560	ESTs	SS,TM
13143	>10	AA436619	ESTs	SS,
36950	>10	AA442050	ESTs	other
36962	>10	AA442082	ESTs	?
36981	>10	AA442845	EST	?
13237	>10	AA443971	ESTs Weakly	?
13242	>10	AA445994	ESTs	other
37057	>10	AA446131	ESTs	other
37068	>10	AA446312	ESTs Weakly	other
37074	>10	AA446344	ESTs	SS,
37084	>10	AA446486	Homo sapiens	?
37135	>10	AA447540	EST	?
37159	>10	AA447714	EST - RC_AA	other
37168	>10	AA447772	ESTs	?
37248	>10	AA449311	Homo sapiens	other
37310	>10	AA451707	ESTs	other
37453	>10	AA454510	ESTs	?
37456	>10	AA454632	ESTs	TM
27787	>10	AA454660	ESTs	?
37492	>10	AA455248	EST - RC_AA	other
37545	>10	AA456841	ESTs	TM
37601	>10	AA458864	ESTs	other
37611	>10	AA458995	Human signal	SS,TM
37615	>10	AA459101	Human serine	other
37653	>10	AA460017	ESTs	other
37677	>10	AA460530	Homo sapiens	other
37777	>10	AA464860	Homo sapiens	other
8648	>10	AA465016	Homo sapiens	?
37816	>10	AA469554	EST	?
37829	>10	AA470094	ESTs	other
28015	>10	AA477421	ESTs	other
37978	>10	AA479294	EST - RC_AA	other
37979	>10	AA479295	ESTs Highly	other
37983	>10	AA479348	H.sapiens m15	other
14054	>10	AA485223	ESTs	TM
38121	>10	AA485724	EST - RC_AA	other
38122	>10	AA485926	ESTs Weakly	other
38167	>10	AA487207	EST - RC_AA	other
38172	>10	AA487424	EST - RC_AA	other
38179	>10	AA487492	Homo sapiens	other
38182	>10	AA487501	ESTs	other
38194	>10	AA487969	ESTs	other
28141	>10	AA488432	ESTs	?
38211	>10	AA488687	ESTs	other
38235	>10	AA489030	ESTs	other
38280	>10	AA489791	EST - RC_AA	other
38316	>10	AA490500	Homo sapiens	other
38330	>10	AA490882	ESTs	other
38456	>10	AA504343	ESTs	SS,
38460	>10	AA504462	ESTs	other

FIGURE 12
(cont.)

38553	>10	AA521471	ESTs	other
38580	>10	AA598545	ESTs	?
38590	>10	AA598648	Human mRNA	other
38601	>10	AA598738	ESTs	?
28323	>10	AA599639	ESTs	other
38828	>10	AA609177	ESTs	TM
38838	>10	AA609215	EST - RC_AA	?
38867	>10	AA609318	Human cbl-b	TM
38871	>10	AA609333	EST	?
38970	>10	AA609749	ESTs	other
38984	>10	AA609839	ESTs Moderat	?
39045	>10	AA610077	ESTs	other
39062	>10	AA620333	EST	?
39080	>10	AA620552	EST - RC_AA	?
39110	>10	AA620709	ESTs Weakly	other
39176	>10	AA621091	ESTs	other
39218	>10	AA621330	ESTs	other
39221	>10	AA621346	Homo sapiens	other
39232	>10	AA621409	ESTs	other
21	>10	AB000905	H.sapiens hist	?
8963	>10	AFFX-HUMT	FAFFX-HUMT	?
33890	>10	AFFX-HUMT	FAFFX-HUMT	?
39302	>10	C14944	ESTs	other
39329	>10	C20797	EST	?
26644	>10	D12163	ESTs	other
218	>10	D13540	PROTEIN-TYR	other
236	>10	D13645	Human mRNA	other
9127	>10	D30037	PHOSPHATID	other
459	>10	D38293	Human mRNA	TM
39405	>10	D50975	ESTs	other
39433	>10	D52037	Human thymid	other
39438	>10	D52692	Human Ca2+	TM
14708	>10	D59388	EST	?
39488	>10	D60831	ESTs	other
39504	>10	D60632	ESTs	other
765	>10	D66096	Prostaglandin	?
787	>10	D66969	Human mRNA	other
789	>10	D66971	Human mRNA	other
39529	>10	F02202	ESTs	?
39535	>10	F02450	ESTs Moderat	TM
18676	>10	F04022	ESTs	other
18718	>10	F04915	ESTs	other
18762	>10	F09458	ESTs	other
18782	>10	F09739	ESTs	other
29080	>10	F13655	ESTs Moderat	other
19001	>10	H02890	ESTs	other
19164	>10	H10395	EST	?
39725	>10	H11323	ESTs	other
19203	>10	H11593	ESTs	other
19328	>10	H17808	ESTs	other
19387	>10	H20128	ESTs	?
39787	>10	H20131	ESTs	SS,
19389	>10	H20165	EST	?
39832	>10	H26279	EST - RC_H2	other
19591	>10	H40688	ESTs	other
29229	>10	H48459	Human mRNA	other

FIGURE 12
(cont.)

19727	>10	H52702	ESTs	?
19787	>10	H56579	ESTs	other
39995	>10	H62474	EST	SS, TM
29331	>10	H68116	ESTs	TM
29344	>10	H68839	EST	?
40064	>10	H72283	Human mRNA	other
40083	>10	H73465	MITOCHOND	other
19949	>10	H78263	ESTs	TM
40204	>10	H88296	EST - RC_H8	other
29523	>10	H88353	ESTs Weakly	?
29551	>10	H90134	ESTs	?
29645	>10	H95840	ESTs	?
20057	>10	H98079	ESTs	other
976	>10	HG2036-HT2	EST - HG2036	?
1158	>10	HG3344-HT3	EST - HG3344	?
1210	>10	HG37-HT37	EST - HG37-4	?
1346	>10	HG4716-HT5	EST - HG4716	?
1349	>10	HG4747-HT9	EST - HG4747	?
1445	>10	J03027	MHC class I p	?
1570	>10	K01383	EST - K01383	?
1684	>10	L07541	Replication fa	other
1852	>10	L17328	Human FE22	TM
1856	>10	L18920	MELANOMA-A	?
1863	>10	L19161	TRANSLATIO	other
2070	>10	L37378	Homo sapiens	SS, TM
2123	>10	L40396	Homo sapiens	other
2144	>10	L41349	Phospholipase	SS,
9723	>10	L44542	ESTs	other
2188	>10	L47276	EST - L47276	other
2343	>10	M15353	Eukaryotic tra	other
2627	>10	M29610	Glycophorin E	TM
2857	>10	M58597	Fucosyltransfe	TM
3021	>10	M68941	Protein tyrosin	other
3163	>10	M84424	Cathepsin E	?
3196	>10	M86917	Oxysterol bind	other
20088	>10	N20054	ESTs Weakly	?
29795	>10	N20641	ESTs Highly	other
40427	>10	N21147	ESTs	other
40444	>10	N22140	ESTs Highly	other
29893	>10	N23003	ESTs	TM
40498	>10	N26086	Homo sapiens	SS,
40559	>10	N33024	ESTs	SS,
30190	>10	N33264	EST	?
30207	>10	N33920	H.sapiens mR	other
20304	>10	N34686	Homo sapiens	?
20307	>10	N34830	ESTs	other
30265	>10	N35115	ESTs	other
40694	>10	N35388	ESTs	other
40604	>10	N38893	Homo sapiens	other
40631	>10	N45124	ESTs	other
40660	>10	N49104	NUCLEAR FA	other
30610	>10	N50138	EST	?
30617	>10	N50946	ESTs	other
30631	>10	N50807	EST	?
30790	>10	N52935	EST	?
20564	>10	N55443	ESTs	TM

FIGURE 12 (cont.)

40760	>10	N57927	ESTs Weakly	other
30938	>10	N58561	Cathepsin B	other
20614	>10	N59230	ESTs	SS,
20657	>10	N62989	ESTs	other
31136	>10	N63512	ESTs Weakly	TM
40627	>10	N64051	Homo sapiens	other
31310	>10	N66831	EST	?
40876	>10	N67607	Human Rho-a	other
20791	>10	N68057	Homo sapiens	?
40905	>10	N68738	ESTs	other
40911	>10	N69114	H.sapiens mR	other
40913	>10	N69218	ESTs	other
31484	>10	N89466	ESTs	other
31619	>10	N73449	ESTs	other
41005	>10	N79516	ESTs	TM
31818	>10	N89774	Homo sapiens	other
31872	>10	N91109	EST	other
41040	>10	N91948	ESTs	other
31944	>10	N93193	ESTs	other
41065	>10	N93818	ESTs	other
32034	>10	N98928	ESTs Moder	other
41107	>10	R01634	ESTs	other
41163	>10	R06176	ESTs	other
21238	>10	R06564	Plasminogen	other
21240	>10	R08613	ESTs	other
21412	>10	R20670	ESTs	other
21519	>10	R27975	EST - RC, R2	other
41381	>10	R42278	H.sapiens mR	?
32169	>10	R43183	ESTs	TM
32195	>10	R43471	ESTs Weakly	other
21902	>10	R43822	EST	?
21946	>10	R44707	ESTs	TM
22072	>10	R49406	ESTs	?
32240	>10	R50976	Ribonuclease	other
32256	>10	R55623	ESTs	other
22256	>10	R56432	ESTs	other
22282	>10	R59197	ESTs	other
32277	>10	R61493	Human mRNA	other
22372	>10	R62831	EST	?
22400	>10	R64109	ESTs	other
41593	>10	R64129	ESTs	other
10233	>10	R71427	ESTs Highly	other
41654	>10	R76437	THROMBOXA	TM
22557	>10	R76722	ESTs	other
22576	>10	R79111	ESTs	other
22593	>10	R79777	EST	?
41678	>10	R80675	EST	?
41719	>10	R89280	EST - RC, R8	other
22793	>10	R96205	ESTs	other
41752	>10	R97063	ESTs	other
3375	>10	S50223	HKR-T1	other
3406	>10	S66596	SQUAMOUS	other
3522	>10	S80287	Spleen tyrosin	other
41793	>10	T03687	ESTs	?
23198	>10	T40530	ESTs Weakly	other
23360	>10	T56531	ESTs	other

FIGURE 12
(cont.)

32635	>10	T61116	ESTs	other
42177	>10	T79786	ESTs	?
23823	>10	T84047	ESTs	?
23662	>10	T86674	ESTs	other
42242	>10	T89579	Homo sapiens	other
23769	>10	T90313	ESTs	other
23832	>10	T92018	ESTs	other
32740	>10	T92950	ESTs	other
42290	>10	T95105	ESTs	?
3598	>10	U01157	Glucagon-like	SS, TM
3659	>10	U04313	Protease inhib	other
3799	>10	U10690	Human MAGE	?
3870	>10	U14518	Centromere p	other
3913	>10	U16261	Human MDA-M	SS,
4029	>10	U21090	Human DNA b	other
4157	>10	U28611	Human cyste	other
4178	>10	U30246	Human burne	TM
15008	>10	U30246	Human burne	TM
4193	>10	U31116	Human beta-5	TM
4306	>10	U36798	Homo sapiens	TM
4362	>10	U39817	Bloom syndr	other
4386	>10	U40622	DNA repair pr	other
4388	>10	U40714	Human tyros	other
4455	>10	U43944	MALATE OXID	other
4477	>10	U45880	Human IAP-like	other
4680	>10	U55766	Human Rev in	TM
4702	>10	U57341	EST - U5734	other
4713	>10	U57721	Human L-tyros	other
4787	>10	U61145	Human enhan	other
4862	>10	U85437	Human homeb	?
4945	>10	U89108	Homo sapiens	other
4975	>10	U71088	Human MEK5	other
4994	>10	U72514	Human C2f m	other
5002	>10	U72761	Human karyo	other
5021	>10	U73524	Human putat	TM
5149	>10	U79716	Human reelin	SS,
5214	>10	U83303	H. sapiens mR	?
5243	>10	U85946	Human brain	other
32789	>10	W02779	ESTs Moder	other
42354	>10	W19346	ESTs	other
42390	>10	W40150	Homo sapiens	other
33006	>10	W46286	ESTs Weakly	TM
33020	>10	W46891	ESTs Weakly	other
33109	>10	W59961	Human mRNA	other
24197	>10	W67277	ESTs	other
24215	>10	W69425	ESTs	other
33301	>10	W73883	ESTs	other
33343	>10	W79634	ESTs Weakly	other
33377	>10	W81219	ESTs Weakly	other
42602	>10	W86423	ESTs	TM
33556	>10	W90705	Murine leukom	other
33616	>10	W93726	Protease inhib	other
33666	>10	W95876	ESTs	TM
3510	>10	X05360	Cell division	?
5558	>10	X07876	Wingless-type	SS,
5603	>10	X14253	Teratocarcin	TM

FIGURE 12
(cont.)

5619	>10	X14850	HISTONE H2A	SS,
5623	>10	X14975	T-CELL SURF	?
5692	>10	X17644	G1 to S phase	other
5789	>10	X54925	Matrix metallo	other
5799	>10	X55330	Aspartylglucos	SS,
5802	>10	X55544	CYCLOC-AMP	?
5857	>10	X58377	Human mRNA	other
5960	>10	X63575	ATPase Ca++	TM
5963	>10	X63629	Cadherin 3 (P	SS, TM
5986	>10	X64810	Proprotein con	?
6041	>10	X67155	MITOTIC KIN	other
6095	>10	X69962	Fragile X mer	other
6106	>10	X70683	SRY (sex dete	TM
6155	>10	X74331	DNA primase	other
6167	>10	X74987	Ribonuclease	other
6188	>10	X76029	NEUROMEDI	TM
6315	>10	X81889	H.sapiens mR	other
6382	>10	X85133	H.sapiens RE	other
6384	>10	X85137	Human kines	other
6438	>10	X89398	URACIL-DNA	?
6449	>10	X89896	H.sapiens mR	TM
6478	>10	X91648	H.sapiens mR	SS, TM
6479	>10	X91653	EST - X91653	?
6494	>10	X92689	H.sapiens mR	TM
6713	>10	Y08564	EST - Y08564	?
6790	>10	Y12394	Homo sapiens	other
24915	>10	YEL003w	EST - YEL003	?
42773	>10	YEL019cMM	EST - YEL019	?
24545	>10	Z38462	ESTs	other
33713	>10	Z39427	ESTs	other
33791	>10	Z40883	ESTs	other
42796	>10	Z99394	ESTs Moder	other
21558	>10	R33112	Human AF-6 m	other
26718	>10	AA282576	ESTs	?
40113	.9855090946	H78003	ESTs	?
10801	.9879448276	AA069285	ESTs Weakly	other
37491	.9513600842	AA455239	ESTs Highly	other
23900	.9272347683	T95789	ESTs	other
254	.9198395324	D14657	Human mRNA	other
6865	.8970827914	Z28331	Ubiquitin-con	other
29693	.8850766396	H97819	ESTs	SS,
26482	.8785189024	AA262491	ESTs	other
23123	.8699502036	T25306	EST	?
26525	.8160399123	AA278392	ESTs	other
13110	.7643256608	AA435840	Homo sapiens	other
34863	.7087597628	AA299784	EST	other
39432	.7034550083	D51691	Phosphoribos	?
31312	.6513325388	N66845	ESTs Weakly	?
21112	.6359446348	R01179	ESTs	?
31572	.6254620695	N71294	ESTs	other
17903	.6221229759	AA180259	EST	?
20747	.6094813734	N66842	ESTs	other
4676	9.589223908	U55206	Homo sapiens	TM
34363	.5627081023	AA251587	Homo sapiens	other
39094	9.540768988	AA620636	ESTs	other
3886	.5372000133	U15128	Human beta-	?

FIGURE 12
(cont.)

39386	9.506250529	D12184	ESTs	TM
7674	4458059039	AA203742	ESTs	other
4192	4329744134	U31059	Human DP pri	TM
4507	9.422674945	U47050	Human putatif	TM
39606	9.412026255	AA402227	ESTs Modera	other
4970	3649551013	U70862	Human nuclea	?
19829	3432151573	H58813	EST	?
14837	2878564114	T40145	ESTs	TM
17336	2822148678	AA099585	ESTs	other
40541	2532836505	N30160	ESTs	other
29496	2487643833	H85434	EST	?
29943	1797074262	N24786	ESTs Modera	TM
17997	1629681314	AA169633	EST	other
21320	1243463318	R11673	ESTs	other
13883	1178796537	AA476917	ESTs Weakly	other
30539	0886687776	N49072	ESTs	other
32778	0877919549	W02063	EST	?
26380	0809559378	AA257012	EST	?
15888	0595893607	X95632	Human Abl int	other
40612	0012674244	N63419	ESTs	other
903	9640387906	D90070	ATL-derived P	other
22674	9515777733	R87160	ESTs	TM
40807	9510132281	N62995	TRANSCRIPT	other
15244	9195644974	W00904	ESTs	TM
32298	8858778587	R87075	Zinc finger pro	other
18269	8575656783	AA209457	ESTs	other
19662	8507626284	H47391	ESTs	other
41607	8.833925517	R67868	CLEAVAGE S	other
2548	8299664893	M25897	Platelet factor	TM
7736	8279341243	AA232121	Human tyrosy	other
34490	7844537272	AA262354	ESTs	other
38658	7889313482	AA599477	ESTs	other
7528	6.765157554	AA149543	ESTs	other
39939	7555031142	H53454	EST - RC_H5	other
25111	7232692306	AA020787	ESTs	other
21655	8.716167279	R38239	EST	?
39663	8.065982652	H04756	ESTs Highly	other
1042	6.652112324	HG2510-HT2	EST - HG2510	?
32330	6361115426	R77776	ESTs	other
25382	6239456467	AA059007	ESTs	other
27074	5900813078	AA401475	ESTs Weakly	SS,
3955	5298909183	U18259	MHC class II	other
4959	8.52646827	U70322	Human transp	other
2315	5259185808	M14123	EST - M14123	?
37253	4896914632	AA449357	ESTs	other
39624	8.471316877	F10836	ESTs	?
23213	4569920887	T40891	ESTs	?
2798	8.455566435	M54955	Connective tis	TM
41154	4413390141	R07499	ESTs	?
32479	4093689543	T16282	WEE1-LIKE P	other
41251	3587565411	R28279	Human clone	other
19081	3583603163	H06701	ESTs Weakly	other
21098	3105627563	R00545	ESTs	other
14723	3061679053	D59894	ESTs	other
37154	299482234	AA447666	Human CENP	other
8068	283568636	AA313387	ESTs Highly	other

FIGURE 12
(cont.)

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7485	8.281679348	AA129547	ESTs	other
16501	2517969834	AA026969	ESTs	other
34527	2419163754	AA279091	ESTs	other
6700	1948675662	Y07867	H.sapiens mR	other
2852	1928816637	M58460	Human 75-kD	other
11188	1862492468	AA172372	ESTs	TM
42293	8.183311064	T95333	ESTs Weakly	TM
5443	176331754	X02530	Interferon (gam	SS,
40937	1534810594	N70607	ESTs	TM
23371	1499496068	T99505	EST - RC T59	?
26272	1339974519	AA252981	ESTs Weakly	other
17306	1332403762	AA086201	ESTs	other
19497	1192326373	AA233795	ESTs	other
235	094436390	D13644	Human mRNA	other
24525	0860187097	Z38347	ESTs	TM
7826	0750029554	AA248584	EST - AA2485	TM
32142	0739258775	R38715	Homo sapiens	other
39087	0557768803	AA620405	ESTs	other
6235	0448957236	X78416	Caselin alpha	TM
29517	0017588724	H65261	ESTs	other
28570	9852455973	C21104	Homo sapiens	other
39344	9182087762	C21034	ESTs Moder	other
19951	9002189759	H00580	ESTs	other
18953	8709180227	H00615	ESTs	other
18376	8584099916	AA225925	ESTs	other
19630	7.847878447	H58911	ESTs	other
36023	7.840635828	AA416881	ESTs	other
13347	8344414516	AA449236	ESTs	other
38614	8284591351	AA431466	ESTs	other
2192	8254072032	L48211	Homo Sapien	?
33016	8006574088	W46577	H.sapiens mR	other
17215	7941954038	AA083044	ESTs	other
34894	7659738108	AA311881	EST	?
40614	7.695001222	N39257	ESTs	other
36295	6634749693	AA424534	ESTs	other
19564	6744302788	H38833	ESTs	TM
16914	6586405336	AA058665	ESTs	SS,
35967	6378079107	AA412694	Human splicin	other
21872	6364823402	R38635	ESTs	other
19918	6303275831	H69787	ESTs	?
10511	6297744492	AA024482	ESTs Highly	other
17721	6057911016	AA136590	ESTs	?
42302	6031859697	T96130	EST	SS,
26134	6000619383	AA243763	ESTs	other
15766	5621799008	F09497	ESTs	other
34492	7.501590494	AA262439	ATL derived P	other
270	4512152125	D14822	EST - D14822	other
35975	4177748986	AA412738	ESTs	other
29842	409580967	N21688	ESTs	?
35389	3913043319	AA399555	ESTs	other
19979	3868157166	H68477	ESTs	other
5793	3865864025	X54942	CDC28 proteol	other
19978	7.380869715	H87770	EST - RC H8	other
1280	3691089318	HG4126-HT4	EST - HG4126	?
31571	3676263454	N71250	ESTs	other
23765	3541191734	T90443	ESTs Weakly	?

FIGURE 12
(cont.)

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35123	.3397933405	AA380927	EST	?
38252	.3341119467	AA489247	ESTs	other
38216	.3282021037	AA489861	ESTs	other
29418	.2489407005	HT7915	EST - RC_H7	?
4834	.1980951054	U63541	Human mRNA	other
42504	.1913035522	W69803	ESTs	other
6111	.7158000198	X71125	H.sapiens mR	TM
41773	.7154479618	T03024	ESTs Weakly	other
9951	.1363626369	N71513	ESTs	other
28109	.0941968224	AA485212	ESTs	other
988	.0783044659	HG2160-HT2	EST - HG2160	?
29848	.0610568511	N22107	ESTs	other
30628	.0607950169	N50744	ESTs	other
22567	.0225726353	R77771	ESTs	TM
9347	.7006323071	H03686	ESTs	TM
11696	.0026773299	AA252894	ESTs	other
40584	.0010096333	N34870	EST	?
193	.9767029198	D10923	PROBABLE G	TM
18305	.9740536051	AA214048	Collagen type	other
6078	.9699682397	X69141	FARNESYL-D	other
26741	.6902658703	AA283198	ESTs	other
35069	.8902855695	AA358397	EST	?
23504	.8977135983	T71042	ESTs	other
289	.8824513023	D16815	Homo sapiens	other
40583	.8689903023	N34855	ESTs	other
31428	.8623762224	N68594	ESTs	other
6169	.8608959727	X75091	SET PROTEIN	other
39524	.8567355171	F01905	MALATE OXID	?
34578	.8430689436	AA280837	ESTs	other
38878	.637527995	AA599520	Small inducib	other
23936	.8251471904	T96830	ESTs	other
9326	.8181321394	D96377	Msh (Drosoph	other
19188	.8067351968	H11255	ESTs Highly	TM
18185	.7882148811	AA194883	Homo sapiens	?
27028	.6757529124	AA399630	ESTs Weakly	other
41289	.751953168	R37265	EST	other
34511	.7364448798	AA278289	EST - RC_AA	?
1566	.7058077710	J05614	EST - J05614	?
25675	.6922997448	AA129757	ESTs Highly	other
5814	.6584342828	X56088	CYTOCHROM	SS.
13861	.6236291801	AA470145	ESTs	other
29794	.6026313355	N20598	ESTs	other
39333	.5902382643	C20910	Cyclin B1	other
3770	.5835303568	J09609	Nuclear factor	other
31831	.5828933784	N88894	ESTs	?
33063	.5808125026	W53000	Homo sapiens	other
20326	.5640084838	N35583	ESTs Weakly	?
34384	.5535703490	AA252537	ESTs	other
25599	.5490481991	AA114091	Human (clon	other
38749	.5366363254	H14988	ESTs	other
42506	.5200567072	W85900	ESTs	?
39808	.5119482188	F10243	ESTs Weakly	?
14617	.5105504748	C14983	ESTs	other
27831	.645670814	AA456044	ESTs	?
34898	.4496517783	AA312551	EST	?
27360	.4434305006	AA425356	ESTs	other

FIGURE 12
(cont.)

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20126	.4326610424N22015	ESTs	TM
6663	.4324809977Y00291	RETINOIC AC	TM
30692	.4196636201N51563	ESTs	other
36472	.4189542286AA428633	EST	?
9578	.3961788753H87652	Homo sapiens	other
39670	.3818496159H05626	ESTs	other
22697	.3652792447R86218	ESTs	other
37308	.3647804993AA461894	EST	TM
16101	.3517262802AA002147	EST	?
20629	.3486854401N59798	ESTs	other
36100	.3364146287AA417740	ESTs	?
15488	.3252580241W28097	Homo sapiens	other
36687	.3131273544AA432136	ESTs	other
30786	.3115037924N52827	EST - RC_N5	?
32882	.2745311453W37683	ESTs	TM
18072	.2675797205AA180448	EST	?
16231	.2652804863AA199747	Human mRNA	other
36282	.2514165676AA469814	EST	?
28125	.6.250317021AA486073	ESTs	other
37484	.2484456362AA454747	ESTs	?
36818	.1948328223AA431478	ESTs	other
5082	.1931116815U78524	Human Gu b1	other
1441	.1777267039J02963	Integrin alpha	other
42105	.6.14875944T67710	ESTs	?
9061	.1394863141X68314	Glutathione pe	SS,
32570	.1156028796T30222	ESTs Weakly	TM
32504	.1019812076T17063	EST	?
23335	.0977927504T56804	EST	?
10857	.0970991073AA068458	ESTs Weakly	other
30883	.0911993489N56923	EST	?
14526	.0859008453AA620295	ESTs	TM
29454	.0865965036H61308	EST	?
8798	.0539173274Y13153	Homo sapiens	TM
21248	.0525428543R08871	ESTs	?
21940	.0499984138RA44538	ESTs	?
29066	.0456247653F10927	Homo sapiens	other
18774	.0446826953F09808	ESTs	?
36722	.017234398AA435512	ESTs	SS,
18062	.0034342366AA179845	ESTs Modera	other
22989	.9992817403T16305	ESTs	other
41745	.9905623808R95856	ESTs	?
8787	.9894877658AA504307	X-LINKED HE	other
20550	.5.984861795N55013	ESTs	other
26470	.9417754101AA262179	ESTs	other
16574	.9356497968AA031926	EST	other
693	.9169537385D90307	Human mRNA	other
4093	.5.814830973U25182	Human antier	TM
1192	.9086254401HG3546-HT3	EST - HG3546	?
22956	.8954735623T10248	ESTs	other
36723	.5.991606409AA435524	EST	?
2114	.8844966598L40384	EST - L40384	other
26872	.5.868238789AA291137	ESTs	other
6602	.8663663016X98266	EST - X98266	other
42701	.8594493433Z39612	ESTs	other
28573	.5.84591116CZ1118	ESTs	other
18290	.8189427595AA211901	ESTs	other

FIGURE 12 (cont.)

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732	804391794	D83781	Human mRNA	other
5330	801414561	U91327	EST - U91327	?
33503	7990715189	W88720	EST	?
2563	779750596	M26167	Human platelet	?
34705	765880625	AA286907	ESTs Weakly	other
42685	759406104	W93659	ESTs	other
38180	7539310793	AA487495	EST - RC_AA	other
4244	747673880	U33286	Human chrom	other
32822	741995745	W16834	ESTs	TM
3977	724588565	U18991	Retinal pigme	?
24673	720236615	Z39301	ESTs	TM
6628	7120261126	Z46626	SRY (sex-dete	other
38726	703079625	AA608733	ESTs	?
39290	689237205	C14573	Human mRNA	other
11405	681887379	AA232231	ESTs	other
22538	679200650	R73567	Homo sapiens	TM
40747	660539320	N56872	Homo sapiens	TM
31596	655402460	N72094	ESTs	other
6329	641585251	X62279	EST - X62279	?
31578	627332368	N71361	ESTs	other
33207	627181848	W70061	H.sapiens mR	other
2545	610586014	M26753	Cyclin B1	other
22560	598840264	R79156	ESTs	other
33592	593514515	W93127	ESTs	other
28843	573469675	D60252	ESTs	other
6160	568905061	X74794	CDC21 HOMO	other
37987	558134588	AA479886	ESTs	other
42515	521788881	W72116	Homo sapiens	other
4732	513068852	U58522	Human huntin	other
3299	509985067	M56523	Hydroxymethyl	?
28320	547340698	AA599574	ESTs	?
746	547126089	D84454	Human mRNA	TM
39373	463590495	C21517	ESTs	other
3117	439841353	M81182	Peroxisomal in	other
21257	434381244	R09196	ESTs Moder	other
31487	431884885	N89507	ESTs	other
28954	413713051	F03153	ESTs	other
38928	538978271	AA809595	ESTs	other
29903	372232062	N23365	EST	?
30925	343743231	N58295	ESTs Weakly	?
19061	334481569	H07864	ESTs	TM
28209	313895191	AA491250	ESTs	other
9470	311889798	H46617	EST - H46617	other
9435	307005685	H30201	EST - H30201	?
28552	295443257	C20914	ESTs	other
27411	294016426	AA428137	ESTs	other
30615	292412526	N60596	ESTs	other
28313	265707716	AA569309	ESTs	TM
35321	264903538	C20632	ESTs	?
25934	253104738	N24194	ESTs	other
1094	249670312	HG2846-HT2	EST - HG2846	?
35578	248112638	F08925	ESTs	TM
11232	246679424	AA186804	ESTs Weakly	other
2486	242634932	M21339	Human small	other
26843	236775868	AA287450	ESTs	?
40331	235338567	H97562	ESTs Weakly	other

FIGURE 12
(cont.)

8035	5.205798365	AA305116	EST - AA305	other
29793	.1955425722	N20593	ESTs Weakly	other
34109	.1481590107	AA210722	EST	?
26408	.1432577257	AA258177	ESTs Weakly	other
19263	.1427029807	H15054	ESTs	TM
24596	.1416089352	Z38810	ESTs	other
28589	.1365059753	C21245	H.sapiens mR	other
5684	.1121931412	X17098	Pregnancy-sp	other
30710	.1079347344	N51761	EST	?
35785	.0973514948	AA406167	EST	?
26360	.0863127861	AA256460	ESTs	?
2351	.0849612092	M15796	Proliferating c	?
30262	.0836877534	N35065	Homo sapiens	other
41792	.0737512468	T03886	ESTs	?
36710	.0703839864	AA434411	ESTs	other
39050	.0546885407	AA620628	ESTs	TM
42185	.0539926381	T79951	ESTs	?
18745	.0460321557	F09134	ESTs	other
35746	.0396841998	AA406063	ESTs	other
35356	.0354809581	AA399053	EST	?
38769	.0312706878	AA435750	EST	?
36900	.0279911548	AA436866	H.sapiens mR	other
27595	.0244757301	AA443326	ESTs	TM
16290	.0056611904	AA016145	ESTs	?
27117	.0016146599	AA405098	ESTs Weakly	other
4304	.9951954397	U36764	Eukaryotic tra	other
33458	.9907402071	W86835	Homo sapiens	other
26693	.9800060678	AA282120	EST	?
12669	.9758136657	AA417030	Homo sapiens	other
29701	.9708526387	H97970	EST	?
20480	.9557253638	N52168	ESTs	TM
8720	.9439110602	AA481218	EST - AA4812	other
34828	.9431269475	AA292436	Homo sapiens	SS, TM
14985	.4941621032	U15128	Human beta-	?
16115	.9377553522	AA004420	ESTs	?
42506	.9348587116	W70074	EST	other
34761	.9310837445	AA287833	ESTs	other
11870	.9281056201	AA262587	ESTs	TM
23211	.9258391854	T40889	ESTs	other
40611	.9180502276	N39138	Homo sapiens	other
42611	.9128605354	W87006	Homo sapiens	other
39652	.9045174605	H03099	ESTs	other
17561	.4889674751	AA129395	EST	?
37239	.8704375389	AA449121	ESTs	?
18712	.8703618781	F04677	ESTs	other
30709	.8611171953	N51752	ESTs Weakly	other
34179	.8503613848	AA227903	ESTs Highly	other
21433	.4825670988	R22183	EST	?
39731	.8186142741	H111760	ESTs	other
31295	.8116614607	N66653	ESTs	other
24647	.4804163055	Z39108	EST	?
31292	.8008871817	N66615	ESTs	other
1285	.7997542393	HG4157-HT4	EST - HG4157	?
1106	.7932425858	HG2981-HT3	EST - HG2981	?
18212	.7912262565	AA168508	ESTs	other
54367	.4782207045	AA251758	Homo sapiens	other

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34802	7797760205AA291468	ESTs	TM
34762	7775301546AA287834	ESTs	other
11595	7696612848AA242819	ESTs	other
8295	7639839111AA405082	ESTs	?
17622	4.758635576AA131584	ESTs Weakly	other
35781	7572463523AA406335	ESTs	other
34754	7483874972AA287642	Human mRNA	other
23237	7444854356T47291	EST	?
37667	728044535AA460318	ESTs Highly	other
11588	7257189975AA236786	ESTs	other
38622	7190695733AA508967	ESTs	?
5137	7057359474U79296	Dihydroliopant	other
25038	7002244726AA010065	CDC28 protei	other
19288	7000147312H16567	ESTs	other
32503	6979486292T17045	Collagen type	other
3278	6953739296M94055	SODIUM CHA	TM
9696	6942061016L38961	Integral trans	TM
35400	6901390896AA399591	Homo sapiens	other
35246	6862691303AA398367	EST Weakly	?
36387	6822499277AA428270	ESTs	other
21509	6730072542R27314	ESTs	other
31381	6729672124N67880	ESTs	other
26723	6727894926AA282781	ESTs Highly	other
36328	6703621086AA425151	Human GAP 5	other
17409	6688418667AA113136	EST - RC AA	other
4908	6552339935U67156	Human mlogb	other
30594	6496238326N49967	ESTs	other
38286	4.84630735AA489847	ESTs Weakly	?
13073	6426509456AA433950	ESTs	other
40435	6240181066N21614	Homo sapiens	other
14474	6226694376AA609427	ESTs Modera	other
38213	4.615309907AA488847	ESTs Weakly	?
5312	4.808644198U80716	Human cell ad	SS, TM
24225	6041590356W70328	ESTs	?
35568	5968982396AA401750	EST	?
29739	5863199051H99626	EST	?
7203	5792982577AA053096	EST - AA0530	other
2157	5772059868L19139	Homo sapiens	SS, TM
32086	5661024279R11510	ESTs	?
8085	5648114736AA314779	ESTs Weakly	SS,
224	5622018989D13633	Human mRNA	other
34006	5609980241AA186761	DNA polymer	other
33696	5557384389W96477	ESTs	other
34065	5537335124AA195517	ESTs Weakly	TM
6028	5357922097U66503	Adenylosuccin	other
4166	5032930671U29463	Cytochrome 5	?
40262	5024727522H93562	ESTs	TM
22687	5018672549R88209	ESTs	TM
41069	4977510482N93989	H.sapiens m	SS,
8284	4793100575AA401334	ESTs	other
27588	4.472017297AA443187	ESTs	other
35882	4717997552AA412047	ESTs	?
34479	4.465519191AA262930	Human tumot	TM
15921	4548516436Y12065	Homo sapiens	?
11279	4380038671AA195399	ESTs	other
38222	4367850785AA621348	ESTs Highly	other

FIGURE 12
(cont.)

34428	.4364736766	AA256526	ESTs	other
8771	4.432067373	AA491188	ESTs	other
22193	.4189610024	R53891	Homo sapiens	other
7898	.4066170674	AA263032	ESTs	other
19902	.3885145805	H66736	ESTs	other
9276	.3865095208	D82374	ESTs	other
10716	.3794529068	AA053319	ESTs	TM
13193	.3751913512	AA442763	ESTs Highly	other
5690	.3723059411	X17620	NUCLEOSIDE	other
35102	4.37147138	AA371509	EST - RC_AA	TM
17983	.3612965467	AA169226	ESTs	other
24962	.3497206925	AFFX-HUMT	AFFX-HUMT	?
31880	.3416539669	N74438	ESTs	other
27168	4.330305894	AA410258	ESTs	other
28731	.3231846655	D20981	EST	?
28348	.3212284908	AA608752	ESTs	other
16335	.3019991487	AA018587	ESTs Weakly	?
33036	.2915644973	W48580	ESTs Weakly	other
30180	.2897721925	N33144	ESTs	other
35591	.2895541242	AA401758	ESTs Weakly	SS,
25340	.2721717135	AA054554	EST	?
28106	.2659103748	AA485084	ESTs	other
38690	.2649184307	AA600121	ESTs	other
20203	.2626499431	N26855	ESTs Modera	other
10251	.2608760694	R76185	ESTs Weakly	SS,
12694	.2604192388	AA417558	ESTs	SS,
31636	.2509469427	N73680	Natural resista	TM
20769	.2479766348	N67277	ESTs	other
1572	.2353281083	K01884	EST - K01884	?
10923	.2292322072	AA116036	ESTs	other
34380	.2283792392	AA252414	ESTs	other
10132	.2222818118	R35733	EST - R35733	other
16629	.2161752118	AA036811	ESTs	other
25146	.1969683794	AA026356	ESTs	?
28730	.1965943098	D20959	ESTs Modera	other
10200	.1874912391	R84521	ESTs	other
38695	.1545794663	AA600176	ESTs	other
31365	4.150549979	N67550	ESTs	other
42379	.1496120668	W37099	ESTs	other
28050	.1428703354	AA470139	Acid phosphat	other
2620	.1386565707	M29474	Human recomb	?
8927	.1340583744	AF008442	Homo sapiens	other
13379	.1269549188	AA449741	ESTs Weakly	other
5134	.1218251808	U79283	Human clone	other
2626	4.1213948	M29581	Zinc finger pro	other
38005	.1160483668	AA479869	ESTs	other
36675	.1127198594	AA431085	EST	?
18296	.1121837207	AA213620	ESTs Weakly	?
29531	.1111456313	H88653	EST - RC_H8	TM
143	.1065880506	AFFX-HUMT	AFFX-HUMT	?
10970	.0967613398	AA129390	ESTs	other
25835	.0952825397	AA152305	interferon (gam	SS,
19735	.0937927853	H53038	EST	?
40711	.0909709431	N53564	ESTs	other
4149	.0901471427	U28386	RAG (recomb	TM
5767	.0882784557	X53793	MULTIFUNCT	other

FIGURE 12
(cont.)

5503	.0861035825	X05232	Stromelysin	SS,
20310	.0541711656	N34893	ESTs Highly	other
456	.059824566	D38145	Prostaglandin	SS,
7814	.0559685676	AA248408	ESTs	other
40230	.0447282719	H90161	ESTs	SS,
33651	4.039204804	W95409	ESTs	other
16777	.0231057929	AA048968	EST	?
19110	.0094905222	H08778	ESTs	other
34442	.0077010365	AA258083	HKR-T1	other
5099	4.004992433	U79247	Human clone	TM
8209	.9990473163	AA384220	ESTs	other
24408	.9976586074	W90146	ESTs	other
28596	.9974919787	AA279943	ESTs	other
16485	.9811264008	AA026269	Spleen focus	other
32969	.9804901745	W42451	ESTs	TM
27006	.9799768093	AA398695	ESTs Weakly	other
29809	.9626765967	N21043	EST	?
9598	.9440163451	H91584	ESTs	TM
29024	.9377933938	F09315	Homo sapiens	other
21694	.9356365584	R39317	Homo sapiens	other
13207	3.925998104	AA443321	ESTs	other
37865	.9143752629	AA478623	ESTs Highly	other
36201	.9128828172	AA421164	ESTs	?
8961	.8981160289	AFFX-HUMTFAFFX-HUMTFA		?
17444	.8927133911	AA115633	ESTs	other
25869	.8919834527	AA157267	ESTs Highly	TM
24862	3.89042252	Z41415	ESTs Highly	other
26855	3.889363206	AA281950	ESTs	?
42300	.8850230386	T95850	ESTs	?
6495	.8830844883	X92715	Zinc finger pro	other
36604	.8828045942	AA598803	ESTs	TM
36358	.8826713718	AA425758	ESTs	other
30560	3.873278445	N49284	MYB PROTO	other
14413	.8724468156	AA600150	ESTs	other
23823	.8574824967	T91805	Homo sapiens	other
38158	3.853096838	AA487021	EST	?
2572	.8519747554	M27281	Vascular endo	other
40100	.8464168967	H75933	Laminin recep	other
40258	.8462992903	H93340	ESTs	TM
20944	.8461821529	N74443	ESTs	other
20411	.8459400966	N48963	Homo sapiens	other
10345	.8457714481	AA001663	ESTs	other
31261	.8451974374	N68248	EST	other
8513	.8378410994	AA446990	ESTs	other
13877	.8363409835	AA476604	ESTs	other
40748	.8253562321	N56879	EST	?
14509	.8152852193	AA609943	ESTs	other
10281	.8065567331	R80333	ESTs	other
25284	.8044158642	AA045074	ESTs Weakly	other
6730	.7900025129	Y09305	H.sapiens mR	other
16033	.7894592402	AFFX-HUMIS	AFFX-HUMIS	?
39242	.7827164808	AA621523	ESTs	other
27354	.7794760436	AA425221	ESTs	?
4552	.3777263005	U49188	Human placen	SS, TM
18385	.7756199108	AA227219	Homo sapiens	other
16754	.7677418053	AA046067	EST - RC_AA	other

FIGURE 12
(cont.)

12752	7671137403	AA421250	ESTs	other
42463	7601033106	W80180	ESTs	other
10614	7581669016	AA037357	ESTs	?
667	7459337509	D87716	Human mRNA	other
7609	7336047135	AA180967	ESTs	other
31795	3732738742	N60703	ESTs	other
36377	7273784603	AA399453	EST - RC_AA	?
22828	7243828524	R98192	ESTs	other
25240	7243198336	AA039713	ESTs	other
11008	7197361366	AA134289	ESTs Weakly	?
4341	7162349944	U38545	Human ARF-4	other
28833	7147618393	D59787	EST - RC_D5	?
3750	7121007154	U09279	Collagen type	SS.
17483	6943413512	AA122147	ESTs	TM
16854	6915208471	AA055552	ESTs Weakly	TM
3709	6891656771	U07550	Heat shock 10	other
1608	6852978422	L00205	KERATIN TY	?
24577	6617721053	Z38727	Homo sapiens	TM
31032	6570916366	N62508	ESTs	other
4961	6536195433	U09546	Human RNA	other
37860	6523276303	AA460225	ESTs	other
20418	6495357091	N49209	ESTs	other
27995	6485167436	AA470155	Homo sapiens	?
7971	6434367186	AA287423	ESTs	other
27606	634303493	AA443763	ESTs	other
24677	6427250833	Z39338	ESTs Highly	other
11070	6408198273	AA148521	ESTs Weakly	TM
9328	6359048598	D89618	Homo sapiens	other
36826	6334689602	AA435996	ESTs	other
17678	6300045792	AA134275	Human HIV1	other
36209	6274694477	AA421268	ESTs Weakly	other
34120	6258090412	AA211615	EST	?
38182	6246442011	AA486737	H.sapiens mF	TM
38463	6164663268	AA504491	ESTs Weakly	TM
20084	6183699976	H98053	ESTs	TM
31256	5992620732	N66152	EST	?
9713	5985228943	L44338	Homo sapiens	other
28622	5768056147	D11837	ESTs	?
38057	5736105703	AA481549	EST - RC_AA	other
28783	5688723791	D45568	EST	?
16996	5680705709	AA069038	EST - RC_AA	TM
28628	5604144817	D11886	ESTs Moderat	?
25804	5442954572	AA148885	ESTs	?
2492	5423954239	M22898	Tumor protein	?
14904	5411970737	T63389	ESTs Highly	other
25265	5347588902	AA043705	H.sapiens RY	other
13606	5327912417	AA456437	ESTs Weakly	other
42307	5315438465	T96595	EST - RC_T9	TM
1544	526202414	J05068	TRANS COBA	SS.

FIGURE 12
(cont.)

Accession	Gene	Protein	Function	Source
C2A8	111929	3.7	A00857	protein (mouse) like 1
BCY2	128790	4.0	AA201725	secreted frizzled-related protein 4
BCY2	101809	5.7	N08845	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBY1	100385	4.8	D78511	mesoderm specific transcript (mouse) homolog
CBY3	102518	2.5	U65832	extracellular matrix protein 1
	134054	6.1	L37006	small inducible cytokine subfamily 5 (Cys-X-Cys); member 5 (epithelial-derived neutrophil-activating peptide 78)
	104209	2.1	AB000221	small inducible cytokine subfamily A (Cys-Cys); member 18; pulmonary and activation-regulated
CJA8	115897	8.1	AA411502	ESTs; Weakly similar to arway tyrosin-like protease (H.sapiens)
	124315	5.4	H94892	v-rat simian leutemia virus oncogene homolog A (ms reliable)
	109415	4.3	AA227218	Homo sapiens CAGP mRNA, partial cds
	103613	5.1	Z46620	SPY (sex-determining region Y)-box 9 (gonopodial dysplasia; autosomal sex-reversal)
	109168	6.2	AA179845	RAB6 interacting; kinesin-like (rakonesn6)
CJA9	115176	5.7	AA463725	ESTs; Weakly similar to KAA2226 (H.sapiens)
CGA7	115522	8.1	AA331383	ESTs
	126852	5.7	H09290	ESTs; Weakly similar to unknown (H.sapiens)
BCN5	112244	3.1	R51309	ESTs
COA1	132692	5.6	AA129390	ESTs
BCN7	117280	5.4	N22107	ESTs; Moderately similar to H ALU SUBFAMILY SC WARNING ENTRY III (H.sapiens)
	102863	4.8	U70322	karyopharin (importin) beta 2
COA2	104600	5.0	AA007180	ESTs
	113702	2.4	T97307	ESTs; Moderately similar to III ALU SUBFAMILY J WARNING ENTRY III (H.sapiens)
	100154	6.0	D14657	KIAA0101 gene product
	102260	3.7	U28386	Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds
	101808	5.7	M08649	Homo sapiens connexin 26 (GJB2) mRNA, complete cds
	133272	3.2	AA465016	ESTs; Highly similar to serine protease homolog
	100365	4.8	U78611	mesoderm specific transcript (mouse) homolog
	126819	4.7	AA305536	EST176522 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence.
	132543	4.6	AA417182	ESTs; Highly similar to protein regulating cytokinesis 1 (H.sapiens)
	103023	5.5	X53793	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase
	132109	3.1	AA598801	ESTs
	104037	3.5	AA372630	differentially expressed in hematopoietic lineages
	104078	3.5	AA068458	ESTs; Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III (H.sapiens)
	108695	3.0	AA121315	ESTs
	107248	3.8	D58694	ESTs
	132802	3.4	AA480869	ESTs
	102104	4.0	W95477	ESTs
	128790	4.0	AA291725	secreted frizzled-related protein 4
	101923	3.8	S75256	HNL=neutrophil lipocalin (human, ovarian cancer cell line OC6, mRNA Partial, 534 nt)
	119843	3.4	W86835	copine III
	130648	3.9	AA075427	ESTs
	132358	3.5	X80466	H4 histone family; member G
	106296	3.2	AA434441	frizzled (Drosophila) homolog 7
	117557	2.3	N33620	disialoglycin
	126691	3.3	X08700	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV; autosomal dominant)
	114787	4.5	AA148885	minichromosome maintenance deficient (S. cerevisiae) 4
	100336	3.8	D63391	platelet-activating factor acetylhydrolase; isoform 1b; gamma subunit (25kD)
	134588	3.5	AA26324	ESTs; Weakly similar to III ALU CLASS A WARNING ENTRY III (H.sapiens)
	110009	3.4	H10933	ESTs
	124058	4.0	F13073	ESTs
	104756	2.2	AA024482	ESTs; Weakly similar to epidermal type I keratin (H.sapiens)
	107151	3.4	AA621169	ESTs
	132669	2.9	AA196378	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN L22 (H.sapiens);
	104334	5.5	H48617	yp19H1.1 Sorens breast 2N4E18 Homo sapiens cDNA clone IMAGE 187521 5', mRNA sequence
	117567	2.5	N32214	ser-Thr protein kinase related to the myotonic dystrophy protein kinase
	104954	3.3	AA074514	ESTs; Moderately similar to (define not available 4753768) (H.sapiens)
	132994	3.7	AA505133	ESTs
	102691	3.7	U72761	karyopharin (importin) beta 3
	103888	2.2	AA314773	ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR (H.sapiens)
	132183	2.5	L19183	Human MAC30 mRNA; 3' end

FIGURE 13A

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118695	3.0	N71781	ESTs
109552	3.4	HG2167-4T22	Protein Kinase 1831, Camp-Dependent
120471	2.5	AA251829	ESTs; Moderately similar to (define not available 4690897) [H.sapiens]
126547	4.2	U47732	transmembrane 4 superfamily member 3
100957	3.3	AA117987	ESTs
129103	4.0	T95333	ESTs; Weakly similar to Strabismus [D.melanogaster]
135243	3.4	AA215333	ESTs
121487	2.5	AA411446	ESTs; Moderately similar to alternatively spliced product using exon 13A [H.sapiens]
131210	2.7	D31058	ESTs
112871	2.4	T17185	ESTs
111179	2.1	N67239	ESTs
123533	2.3	AA608751	ESTs; Moderately similar to III ALU SUBFAMILY SC WARNING ENTRY III [H.sapiens]
105175	2.4	AA185804	ESTs; Weakly similar to unknown [S.cerevisiae]
105156	2.7	AA172372	ESTs; Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]
111223	2.5	N68921	ESTs; Weakly similar to neogenin [H.sapiens]
132150	2.7	AA105569	Ribonuclease activation protein; alpha
105400	2.1	AA447521	ESTs
129260	3.1	AA053634	ESTs; Highly similar to (define not available 4679014) [H.sapiens]
115291	3.9	AA278943	ESTs
128528	2.1	C14037	ESTs; Weakly similar to Yel007c-ap [S.cerevisiae]
116399	2.7	AA559726	Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds
130887	3.5	R49698	ESTs
105082	2.6	AA143763	ESTs; Weakly similar to Similarity to S. Pomila BEMVBD5 suppressor [C.elegans]
103453	3.2	X89565	H.sapiens mRNA for SMT36 protein
115847	2.6	AA443793	ESTs
105012	2.8	AA115036	ESTs; Highly similar to (define not available 4589929) [H.sapiens]
105507	3.2	AA264978	ESTs; Moderately similar to (define not available 4106061) [H.sapiens]
130800	2.6	AA221386	ESTs; Weakly similar to katanin p80 subunit [H.sapiens]
116481	3.4	AA821557	ESTs; Moderately similar to III ALU SUBFAMILY SQ WARNING ENTRY III [H.sapiens]
129945	2.5	AA232104	ESTs; Highly similar to (define not available 4329579) [H.sapiens]
100864	2.1	HG4297-IT49	transcriptional Coactivator Pct4
128131	2.3	A283102	claudin 3
131664	2.8	AA491455	ESTs
100279	3.1	D42084	Human mRNA for KIAA0094 gene; partial cds
134405	1.8	J04177	collagen; type XI; alpha 1
130287	2.6	AA113149	tumor suppressing nontransferable candidate 3
108828	2.1	AA131804	ESTs; Weakly similar to coded for by C. elegans cDNA on 16K [C.elegans]
131269	2.2	AA495897	ESTs
108141	4.2	AA176428	ESTs
119307	2.5	T32108	ESTs
134319	2.1	AA129547	ESTs; Moderately similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
133458	5.0	M18728	non-specific cross reacting antigen
116732	2.3	F13779	ESTs; Weakly similar to III ALU SUBFAMILY J WARNING ENTRY III [H.sapiens]
115239	3.0	AA278650	ESTs

CGAS

FIGURE 13B

Code	PRIMER KEY	Clonotopology	Accession	Comments
CZAB	111929	3.7	R40057	prominin (mouse)-like 1
BCX2	128750	4.0	AA291725	secreted frizzled-related protein 4
CBG2	101809	5.7	M86849	1 homo sapiens connexin 26 (GJB2) mRNA, complete cds
CBG1	100365	4.8	D79611	mesoderm specific transcript (mouse) homolog
CBG3	102618	2.5	U55932	extracellular matrix protein 1
CJA8	115997	8.1	AA411502	ESTs. Weakly similar to airway trypsin-like protease (H sapiens)
CJA9	116176	5.7	AA463725	ESTs. Weakly similar to KIAA0226 (H sapiens)
CGA7	115522	8.1	AA331393	ESTs
BCN5	112244	3.1	R51309	ESTs (now Sulfatase by in-house sequencing)
CQA1	132592	5.6	AA129390	ESTs
BCN7	117260	5.4	N22107	ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! (H sapiens)
CQA2	104650	6.0	AA007160	ESTs

FIGURE 14

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TGTGTTGTTTATTTACCCCAATTCAAGTTGACAACTGAGGCAACGCAAGCTCCAGTCTCCAATAAGAAACCAAGTGTGATCTTA
 AAGCAAGTTTGTCTGTCGCCCTCAACTATGAACCAACAAAGGAAAGCTAAAACCATGGGGCAATCTAAGAAATAATAT
 TATCTAAATCAACATGTCACAGAAATTAAGTCTACAGAAAGAACTTACAAACACCCCATCTCCAGACAAAGGAAAGCA
 ACGGAAAGAAAGGCAAGGAGAAAGGAGAAAGGAAAGGTTGGGAATGCGAAGGGGCTCATTGTGGCTGAAG
 ATCTGCTGAAAGACGTTATCACCTTAAAGCTCAAATTTCTGGATGGTTTTTACTTAAAGTCCATTAAACAATTCAGGTTT
 GTAACGAGACCCATCTAAATTTCTGTTCTAGATTTTAAATGTCAAGTTCCCAAGTTCCCTCTGCTGTTCTAATATTA
 ACAGAACTGCAGTCTCTGCTAGCCCAATAGCAATTACCTGATGGCAGCTAGTTATGCAAGCTTCAGGAGAAATTTGAACA
 TAACAAGAAATAGGTAAGCTGGGATAGAAAGGCCACCTCTTCACTCTCTATAGAATATAGTAACCTTTATGAACGGGGC
 CATATAGTTTGGTTATGACATCAATATTTACCTAGGTGAATTTGAGGCTTATGTACCTTCGTTCAAAATATCTCAT
 GTAATTGCCATCTGTCACTCACTATATTCACAAAAATAAATCTTACACCTCATCTCAACATTGCTTACTTAAAGCTAC
 ATAGCCCTATCGAAATGCGAGGATTAAATGCTTTAATGCTTTTAGAGACAGGGTCTCACTGTGTTGCCAGGCTGGTCTCA
 AACTCCACCAATATGACTTCTTATTCAATTTATGGAAAGACTAGGCTTTGCTTAGTATCATGTCCATGTTTCTCTTCACT
 TCAGTGGAGCTTCTGAGTTTATATCTGCTCAAGATCGTCATAAATAAATTTTCTCATTTGTCAAAAAATAAAAA
 AAAAAAAAAAAAAA

FIGURE 15

ATCCATGATTACGCCAAGCTTGGCAGGAGGAGACAGCCACTTGGCCATGTCACCAAAACAAGGAGAAGGTGCAGAG
TGTCGGTGTGGACCTGACTCACAGCAGAATCATTGAGAGATAAAAAATAAGT/ATCCCACCTGAATTCAGAAATCATGAAA
AGCAGGAAAGCCAGGATCTCAGAGCTACTGCCAAAGTTCTCTCCACCAGACGAGCACCAGAAGCTGAGAAATGCTGTT
TCCTCAGGTAACAGAGATTCAAGGTACCTTCAGAGGAAAGAAATCTCTCTACACAGATGAGTCATCCAAACCTGGAAA
AAAT/AAAGAACTGCAATCACTACTCCAACTTTAAGAAAGCTTCATGAAGCTCATTTAAGGAAATGAGTCCATTGATC
AATATATTGAGAGAAAAAGAAACATTTGAGAAACACAATTCATGAATGAAGTGAAGCAGCAGCCCATCAAT/AAAGGA
GGGGTCAGGACTCCAGTACCTCCAAAGGAGAGACTCTCTGTGCTTCTACTCCCATCAGCAGCAGCCTCGCAAGGCCG
GTCTTGTGGCCCTGCAAGTCAGAGTACCTTGGGTCTGAAGGGGTCACTCAAGCGCTCTGCTATCTCTGCAGCTAAACGG
GTGTGAGGTTTTGAGCTGCTACTAAAGATAATGAGCAT/AGCGTTCACTGACCAAGACTCCAGCCAGAAAGTCTGCACAT
GTGACCGTGTCTGGGGGCACCCAAAAGGCGAGGCTGTGCTTGGGACACACAAATTAAGAGACCATCACGGGGAAATCTGC
TGCTGTTATTACCCATTCAAGTTGACAACCTGAGGCAACGAGACTCCAGTCTCCAATAAGAAACCAAGTGTGATCTTA
AAGCAAGTTTGTCTGTCCTTCACTATGAACCACACAAGGAAAGCTAAACCATGGGGCAATCTAAGAAATAAT
TATCTAAATCAACATGTCAACAGAATTACTTCTCAAGAAACTTACAACAACCCCATCTCCAGACAAAGGAAGACA
ACGGAAGAAACGCGAGCAAGAACGAAGGAGAGAAGCAAGGTTTTGGGAATGCGAAGGGGCTCATTTTGGCTGAAG
ATTTT

FIGURE 16

MTMITPSLARGRQPLGHVTKTRRRCKTVRVDPDSQQNHSEIKISNPTEFQNHKEQESQDLRATAKVSPSPDERQEENAV
SSGNRDSKVPSEGKKS LYTDESSKPGKNKRITAITPNFKKLHÉAHFKEMESIDQYIERKÑKHFEHNSMNELKQQFINKG
GVRTPVPPRGRLSVASTPISQRRSQGRSCGPASQSTLGLKGS LKRS AISAAKTGVRFSAATKDNEHKRSLTKTPARKSAH
VTVSGSTQKGEAVLGTHKLKTIITGNSAAVITPFKLITEATQTPVSNKKPVFDLKASLSRPLNYEPHKGK LKFWGQSKENN
YLNQHVNRINFYKKTYKQPHLQTKEEQRKKREQERKEKKAKVLGMRRLILAED

FIGURE 17

Amino-CKVLG MRRGL ILAED-COOH

FIGURE 18

Acetyl-KQPHL QTKEE QRKKC-Amide

FIGURE 19

```

human_CAA2 -----KKHFEIHSNMLKQPIKGGVRTVPVPPGRISVASTPISORRS
mouse_CAA2 ARFKKMESIDEYIMAKKKHILKEHSSLNELKLDK--GIVTPVPPFGRISVPTPARQQCP
          *:..*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
human_CAA2 QGRSCGPASOSTLGLKGLKRSASAAKTGVRFSAATKDNEHKRSLTKTPARKSAHVTS
mouse_CAA2 QG-----H--S-ATKMNVRISAATKDNEHKCSLTKTPARKSPHVTAP
          *:..*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
human_CAA2 GGTQKGEAVLGTHKLKLTIGNSAAVITPFKLTTEATQTPVSNKKPVFDLKASLRPLNYE
mouse_CAA2 GSASKGQAVFRTPKSKATERTSIAVITPFKLTTEATQTPSSSKKPVFDLKASLRPLNYK
          *:..*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
human_CAA2 PHKGKLPFWGQSKENNYLNQHVNRINFYKKTYYKQPHLOTKEEQKKRQEQRKEKKAKVLG
mouse_CAA2 PHKGKLPFWGQAKENNSLNERVSRVTFHRKTYKQPHLOTREERWKRRQEQRKEKKKLE
          *****:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
human_CAA2 MRRGLLAED-
mouse_CAA2 ARRNGLGVTKAQ
          **.* : :

```

FIGURE 20

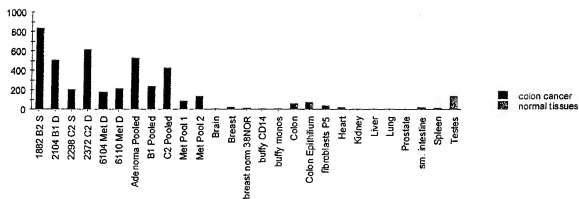


FIGURE 21

FIGURE 22

GGTGGCCCTCTGTGGCCGTCCAGGCTAGCGCGCGGCCCGCAGCGCGCGGGAGAAAGACTCTCTACCTGGTCTTGCGGCTG
 TGCCACCCCGCCGCAAGGGTGTGGAGGGCGTGCTGCCGAGACCTGCCCGGGCTTCGGGAGACCGCGTCAAGCCGCTG
 AGCTATGGAGCCCGCGCCACCGCGCCCTCTCTCCGGCGCCCGGAGACTGGCCGGGTTCGGGAGACCGCGTCAAGCCGCTG
 CGCTGGCCGACGCGAGGGTGGAACTGCCCGGACCGCGTGTGCCCTCGGTGCCGAGAGATGTCTGCCCGCCGAGCCGGGAC
 GCGCGCGGGGTGCGGATAGGGGCCCCGCGCGCGCGGGGACGGGTGGGACAGCCCTTGGGGCCACCCCGAGCCGACAG
 CCGTTTCCAGTGGACCTGGTTTCCGAGAACCGCGCGCGGGCGGCTGTCTGCGCGCGGGCGCGCGCGCGCGGACGCGCGG
 CGGCTGTGCTGGGGCGGGGGCCAGCAGACCCCCGCGGACGGGGAAGCCAGCGCGAGAGCGAGCCAGCTAAAAGGCA
 GAGGAAGCCAAAGGCCGCTTCCGCGTGAACTTCTGGAGCCAGCTGCCCTCTCGTGGTGAAGACAGCTGTCTAGATGC
 TGCCCGGGTGGAGTGCAGCGGCCCAACGTGAGCTTCCAGAACGCGCGGGACACGGTCTGAGCGAGGCGAGCAGCTGT
 ACTCCGCGCGCGCGCGCGCGCAGTGGGACCCAGCAGCACTATTATGATACCCACACCAACCTACTACTCTGCCGAC
 TTCCGCCCAACACCATGGAGCGCTGTGCCAGGATCGATCACTACCGGCACACAGCCCGCGCAGCTGGGCGAGAAAGCTGTCT
 CCGGCCCTAGCTTGGCGGAGCTCCACGACGAGCTGGAAAAAGGAACCTTTTGGAGATGGCTTTGCAATGGGGAAAGAAAT
 CTCACACAGAGATGCTGTGGTCACTGATATCGCAGAAAGTAAAGGAGCTGTGAAGTTTGGCTGGATCAAGGGTGTATTA
 GTACGTTGTATGTTAAACATTTGGGGTGTGATGCTTTTCATTAGATGTGTCATGGATTTGGGTCAAGCTGGAAATAGGTCT
 ATCAGTCTCTGTAATAATGATGGCCACTGTTGTGACAACTATCAGAGATTGTCTACTTCAGCAATAGCAACTATGGAT
 TTGTAAGGAGGAGGAGGCATATTTAATATCTAGAAGCTTAGGGCCAGAATTTGGTGGTGCAATTTGGTCTAATCTCTC
 GCCTTTGGCAACGCTGTGGAGTGTCTATGTATGGTGGATTTGAGAAACCGCTGGTGGAGTTGCTTAAGGAACATTC
 CATAGTTATGATAGTGAATCAATGATATCCGAATTTATGGAGCCATTAAGTGTGATTTCTTTAGGATCTCAGTAG
 CTGGAATGGAGTGGGAAGCAAAAGCTCAGATTTGCTTTTGGATCTCTAATCTCTGGTATTTGGTATTTGCTCATAGGA
 ACAATTTATCCACTGGAGAGCAAGAACCCAAAGGGTTTTTGGTTATAAATCTGAATATTTAATAGGAACCTTTGGGCG
 CGAATTTTCGAGAGGAAGAGACTTTCTTTCTGTATTTGCCATCTTTTTTCTGCTGCAACTGGTATTTCTGCTGGAGCAA
 ATATCTCAGAGATTTGCGAGCTCTCAGTCAGCCATACCCAAAGGAACACTCTCAGCATTTTAATTAATCATTTGGTT
 TACGTAGGAATTCAGATATCTGTAGGTTCTTGTTGTTGTCGAGATGCCATGGAAACGTTAATGACATCTGTGTGAAGCA
 GCTAACAAACTGATCTCTGCGAGCTGCAAAATTAACCTTTGATTTTTCATCTGTGAAGACGAGCTGTTGCTCATTTGCC
 TAATGAACAACTTCGAGTAAATGATGATGTTGTGTCAGGATTTACACCACTAATTTTTCGACGATATATTTTCAGGACACTCTT
 TCTTCAGCATTGACACTCCTGATGATGCTCCCAAAATATTTTCAGGCTCTATGTGAAGGACAACATCTACCCAGCTTTCCA
 GATGTTTGCTAAAGGTTATGGGAAAAATTAATGAACCTCTCTCGGCTCATCTTAACTTTCTAATTTGCACTTTGGATTCA
 TCTTAATTTGCTGAATGATTTATTCACCAATTTATCTCAAACTCTCTCTTGCACTCATGATGATGATCAATTTTCTCA
 GTATTCCTGATGCTGATTCGAAATCTCCAGGATGGCGTCTGCAATTCAAATCTACCAACATGATGGGATATCACTTTCTGG
 AGCAATTTCTTGTCATATGATGTTGCTGATTAATGTTGGGCTGCAATGCTAACATGATGATGATGCTTTGGGCTGT
 ATATTTATGTTTACCTACAAAAACCCAGATGTGAATTTGGGGATCTCTTACACAGGCCCTGACTTCTGATGATGATGATGATGAT
 CATTCAAATTCGCTTTCTGGAGTGGAGACCCAGTGAAGAACTTTAGGCCACAGTGTCTTTGTTATGACAGGCTGCTCCAAA
 CTCAGCTCAGCTTTTACTTCTATCTGTTTCATGATTTTCAAAAAAATGTTGGTTTGTATGATCTGTGGCCATGTACATATGG
 GTCTCGAAGACAAGCATGAAAGAGATGTTCCATCGATCAAGCCAAATATCAGCAGTGGCTTTATTAAGACAAATGAAG
 GCATTTATGCTCCAGTATCATGCAAGATGATCTGAGAGAAAGTGCAAGATATTTGATGCAAGCTGCTGTGTTCTGTGTAT
 GAAGCCAAACACACTGTGCTTTGGATTTAAGAAAGATTTGGTTGCAAGCAGATATGAGGAGATGTGGATATGATATATAACT
 TATTTTCATGATGCTTTTGACATCAATATGAGATAGTGGTTATTCGCTTAAAGAAAGGTCTGATATATCTCATCTTCAA
 GGACAAAGAGGTGCTGTGTGCTCATCAAGAGAAATCTCTCGCCCAAGAGATGTGGTGAAGTGTGGAAATAGTAAAAAT
 GTCCGATTTGATATCTTCCAAACCACTCAGTGAAACCAATATACACAAGAGTGGAGAGAGAGATGGCAGACCTGCA
 CTCACCAACTGTTGGAATGAAATCCAAAGGCCATTTGTCCTTTAAATGTAGCTGACAAAGAGTCTTTGAGACTAT
 ACACAGTTTTCAGAAAAACCAAGGAAAGAAATACTATTGATGTCTGGTGGCTTTTGTATGATGGAGGTTTGACCTTATGAT
 ACCTTACCTTCTGACGACCAAGAAAAATGGAAAGACTGTGAGATCAGAGATTTATCTGATGGAAGATTAACAGAAATAG
 ACCATGACCGGAGAGCATGGCTACTTTGCTTACGAAGTTCGGATAGAGACTTTCTGATGTCAAGTCTTAGGAGATATC
 AATACCAACCAAGAAAGAAATATATAGCTTTTGGAGAAATCATGAGCCATACAGACTTCATGAAGATGATGAAGAA
 GAGAGATATTGACAGTAAATGAAGAAAGATGAACCTGCGGAATTAACAGATTAAGGCTTGAACATTTATTAAGACCAAGA
 CATACCGGACAGATCAGGTTAAATGAGTTATTAAGGAACATTCAGACAGAGTATATATTTGTCATGAGTCTCCAGTT
 GCACAAAGAGGTGCTGTGTGCTGCTCTACATGGCATGGTGAAGAGCTTACTAAGAGCACTACCAACCTCTCTCT
 AGTTGCTGGGAATCATCAGAGTGTCTTACCTCTTATTCTAATGTTCTATAGCGTGACAGCCCTCCAGATGGTATCT
 TCAAGTGGCTAGTGTAGTAAACCTGAAATCTCAATGACACATTAACATCAAGTACGGAATGTGAGATCTTTCTTCTTCAGAT
 TCTATTAAATTTGAAGACACACAGGAAAGCTTGTCTCATGATAAGCTGTATGAGAGCTCTGGTTTGTAGTCAATTCATAT
 CTCAATCTTAAGTGTATCTCTCTCTGTTGAATGAAGTTTGTGAGAGTATTTTCTCTTGCTACTTGAATAGCAATAAA
 AGCGGTGTTAACTTTTGG

FIGURE 23

ATGAGGCCGCGGCCACGGCGCCCTCCTCCGGCGCCCGGGAGCTGGCCGGGGTCGGGGAGACGCCGCTCAGCCGCTGCGCT
 GGCAGCAGCCAGGGTGGAACTGCCCGCACGGCTGTGCCCTCGGTGCCGAGGATGCTGCGCCGCGAGCCGGAGCGGG
 GCGGGCTCCGCGATGAGGGCCCCCGCGCGCCCGGGGACGGGCTGGCGAGACCTTTGGGGCCCCACCCGAGCCAGAGCGT
 TTCCAGGTGGACCTGGTTCCCGAGAAGCGCGGGCGGCCGCTGCTCGGGCGCGGGCGCGCGCGGCGCAGCGCGCGCGG
 TGGTCTCGGGGCGGGGGCCAAAGCAGACCCCCCGGACGGGGAAGCCAGCGCGGAGAGCGAGCCAGCTAAAGCAGCGAGG
 AAGCCAGGGCCGCTTTCCGCGTGAACCTTCGTGACCCAGCTGCCCTCTCGTGGCTGAAGACAGCTGCTCAGATGCTGCC
 GGGGTCGGAGTCGACGGGCCCAACGTGAGCTTCCAGAACGGCGGGACACGCTGCTACGGAGGGCAGCAGCTCGCACTC
 CGGCGCGGGCGCGCGAGTGGCACCACCGAGCACTATATTATGATACCCACCAACACCTACTACTCGTGGCGACCTTCG
 GCCAACACCATGGACGCTGTGCCAGGATCGATCACTACCGGCACACAGCCGCGCAGCTGGGCGGAAGCTGCTCCGG
 CCTAGCCTGGCGAGCTCCACGACGAGCTGGAAAAGGAACCTTTTGAGGATGGCTTTGCAAAATGGGGAAGAAAGTACTCC
 AACCCAGAGATGCTGTGGTCACGTATCTGCAAGAAATGAAGGAGTCTGGAAGTTTGGCTGGATCAAGGGGTGATTAGTAC
 GTGTGATGTTAAACATTTGGGGTGTGATGCTTTTCATTAGATTGTCTAGGATTGGGGTCAAGCTGGAATAGGTCTATCA
 GTCTTGTAAATGATGAGCCACTGTTGTGACAACTATCACAGGATTGTCTACTTCAGCAATAGCAACTAATGGATTGT
 AAGAGGAGGAGGAGCATATTATTAATATCTAGAAAGTCTAGGGCCAGAAATTTGGTGGTGAATTTGGTCTAATCTTGCCCT
 TTGCCAACGCTGTTCAGTTGTCTATGTATGTGGTTGGATTGTCAGAAACCGTGGTGGAGTTGGCTTAAGGAACATTCCATA
 CTTATGATAGATGAAATCAATGATATCCGAATATTGGAGCCATTACAGTGTGATTCTTTTAGGTATCTCAGTAGCTGG
 AATGGATGGAGCAAAAGCTCAGATTGTTCTTTTGGTGATCCTACTCTTGCTATTTGGTGATTTCGTCAAGGAACAT
 TTATCCCCTGGAGAGCAGAAAGCCAAAAGGGTTTTTGGTTATAAACTGGAATATTAATGAGAACTTTGGGCGCGAT
 TTTCCGAGAGGAAGAGACTTTCTTTTCTGATTATTTGCCATCTTTTTCCTGCTGCAACTGGTATCTTGGCTGGAGCAAAAT
 CTCAGGTGATCTGCGAGTCTCTCAGTCAGCCATACCCAAAGGAACACTCTAGCCATTTTAATTACTACATTTGGTTACG
 TAGGAATTCAGTATCTGAGGTCTTGTGTTGTTGAGATGCCACTGGAAACGTTAATGACACTATCGTAACAGAGCTA
 ACAACTGTACTTCCGAGCCTGCCAAATTAACCTTTGATTTTTCATCTTGTGAAGCAGTCCCTTGTCTTATGGCCATTAAT
 GAACAACTTCAGGATATGAGTATGCTGTCAAGATTACACCACTAATTTGCGAGGTATATTTTCAGCCACTCTTTCTT
 CAGCATTAGCATCTCTAGTGAGTGTCTCCCAAAATATTTCAGGCTCTATGTAGGACAACACTTACCAGCATTTCCAGATG
 TTTGCTAAAGGTTATGGGAAAAAATTAATGAACCTCTCTGTGGCTACATCTTAACATTCTTAATTGCACTTGGATTCACTT
 AATTGCTGAACCTGAATGTTATTGCAACAAATTATCTCAAACCTTCTCTCTGCTCATATGATATGATCAATTTTCAGTAT
 TCCATGCTACACTTGCAGAAATCTCCAGAGATGGCGTCTGCATTTCAAATACTACAACATGTGGATATCACTTCTGAGCA
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 CAATTTGCTCTTTCTGGAGTGAAGACCAAGTGAAGAACTTTAGGCCACAGTGTCTTGTATGACAGGCTCTCCAAAGTCA
 CGTCCAGCTTTCTTCATCTTGTTCATGATTTCACAAAAAATGTTGGTTTGTATGATCTGTGGCCATGTACATATGGGCTC
 TCGAAGATACCCGCTGAAGAGATGTCCTCATGATCAAGCCAAATATCAGCGATGGCTTAATAGAAACAAATGAAGGAT
 TTTATGCTCCAGTATCATGAGATGACTTGAGAGAAGGTGCACAGTATTGATGACGGCTGCTGCTTGTGCTGTATGAAG
 CCAACACACTGCTCTGTTGATTAAAGAAAGATTGGTTGCAAGCAGATATGAGGATGGGAATGTATATAAACTTAT
 TCATGATGCTTTTGACATACAATTGGAGTAGTGGTTATTTCGCTTAAAGAAAGGTCTGGAATATCTCATCTCTCAAGAC
 AAGAGAATTTATTGTCATCAAGAGAAATCTCCTGGACCAAGGATGTGGTAGTAAGTGTGAATATAGTATAAAGAGTCC
 GATTGTAGATTCTTCCAAACCATCTCAGTGAAGAAACCAATTACACAUAAGTTGAGGAAGAGGATGGCAAGACTGCACTCA
 ACCACTTGTGAAGAACAGATTCCAAAGGCCCTATTGTGCTTTTAAATGAGTGTGACCAAAAGCTCTTGAAGCTAGTACAC
 AGTTTTCAGAAAGAACAGAAATACTATTGATGCTGTGGTCTTTTGTATGATGAGGTTTGTACCTTATTGATACCT
 TACTCTTGACGACCAAGAAATAATTATGCTTTTGTAGGAATCAATGAGCTACAGATATTCTATGGTGAAGATAACACAGATTGACCA
 TGACCCGAGAGCGTGTACTTGTCTAGCAAGTTCCGGATAGACTTTTCTGATATCATGGTTCTTAGGAGATATCAATA
 CCAAAACCAAGAGAAATAATTATGCTTTTGTAGGAATCAATGAGCTACAGACTCTAGAGATGATAAAGAGCA
 GATATTGACAGATAAATGAAGAGATGAACCATGGCAATACAGATAATGAGCTTGTACTTTATGAAGCAACAGACATA
 CCGGCAGATCAGGTTAAATGAGTTATTAAGGAACACTTCAAGCACAGCTAATATTATGATCTAGAGTCTCCGAGTGTGAC
 GAAAGAGTGTGCTGTAGTGTCTTCTCATGGCATGGTTAGAAGCTTATCTTAGGACCTACCACCAATCTCTAGTT
 CGTGGGAATCATCAGAGTCTCTTACTTCTATTCTAAT

MEPRPTAPSSGAPGLAGVGETPSAAALAAARVELPGTAVPSVPEDAAPASRDGGGVDEGPAAGDGLGRPLGPTPSQSR
 FQVDLVS ENAGRAAAAAAAAAAGAGAGAKQTPADGEASGESEPAKGSEAKGRFRVNFVDPAASSSAEDSLSDAA
 GVGVDGPNVFSQNGGDTVLS EGSSLHSGGGGSGHHQHYYDDTHINTYYLRTFGHNTMDAVPRIDHYRHTAAQLGEKLLR
 PSLAELHDELEKEPFFEDGFANGEESTPTRDAVVITYAESKGVVKGWIKGVLVRCMLNINGVMLFIRLSNIVGQAGIGLS
 VLVIMMATVVTITGLSTSAIATNGFVRGGGAYYLISRLGVEFGSAIGLIFAFANAVAVMYVVGFAETVVVELLKEHSI
 LMIDEINDIRIIGAITVVVILGISVAGMEWEAKAOIVLLVILLAILITTLVYVGIAVSVGS CVVRDATGNVNDTIVTEL
 FREEETFFSVFAIFFPAAATGIIAGANISGDLADPQSAIPKGTLLAILITTLVYVGIAVSVGS CVVRDATGNVNDTIVTEL
 TNCTSAACKNLFDFSSCESSPCS YGLMNNPQVMSMVSGFTPLISAGIFSATLSSALASLVSA PKIFQALCKDNIYPAPQM
 FAKGYGKNNELRQYILITPLIALGFIILAEINVIAPILISNFFLASVALINFSVFHASLAKSPGWRPAPKYNNMILSLGA
 ILCCIVMEVINWMAALLTYVIVLGLYIYVTVKKPDVNWGSSTOALTYLNLALQHSIRLSGVEDHVKNFRPQCLVMTGAPNS
 RPALLHLVHDFTKNVGLMICGHVHMGPRRQAMKEMSIDQAKYQRWLIKNNKMAFYAPVHADDLREGAQYLMQAAGLGRMK
 PNTLVLFQFKDWLQADMVDVMYINLFHDAFDIOYGVVVIRLKEGLDISHLQGOEBELLSSQESKSPGTKDVVVSVEYSKKS
 DLDTSKPLSEKPIITHKVEEEDGKTATQPLLEKESKGPVPLNVADQKLEASTQFQKKQGNITIDVWMLFDDGGLTLLIP
 YLLTTKKKWKDCKIRVFIGGKINRIDHRRAMATLLSKFRIDFSDIMVLGDINTKPKKENIIAFEIIIEPYRLHEDDKEQ
 DIADKMKDEPWRITDNELELYKTKTYRQIRLNEILLKEHSSANIIVMSLPVARKGAVSSALYMAWLEALSKDLPILLY
 RGNHQSVLTFYS

FIGURE 24

FIGURE 25

Peptide names	Solubility	
CAA9p1	1mg/1ml H ₂ O	H-CDPAASSSAEDSLSD-NH ₂
CAA9p2	1mg/1ml H ₂ O	Ac-KKSDLDTSKFLSEKC-NH ₂
CAA9p3	1mg/1ml H ₂ O	Ac-PLKKKESKGIIVFLC-NH ₂
CAA9p4	min.aml.DMSO/H ₂ O	Ac-EHSLHIDEIC-NH ₂
CAA9p4MAPS	1mg/ml buffer pH7.5	Ac-EHSLHIDEIC-on 8-Branch Maps
CAA9p5	1mg/1ml H ₂ O	Ac-DFREEETC-NH ₂
CAA9p5MAPS	1mg/1ml H ₂ O	Ac-DFREEETC-on 8-Branch Maps

FIGURE 27

GGCAGCGAGGAGAACTTAAAGAAATTGAGATATGTGAAGTGTATTCAGGAAACCTCGTCA
 TCCTCTGTATGACAGTTGTGACAGCTTTGCTTCTGTATAAATTTTGCAAAACGAGGGCTGCAGTCA
 GTTCGGGAAAGGCTGTAGGACCCGACGCACTGTGAGGCACTCTGGAOCTCTCAGGCTGGGCGAT
 GAAAGTATTCACGCGCGAGTACCAAGGGAGCAACCAACAAAAAGCAGAGTCCCGCCAGCCCT
 CAGAGAAATCTGTGACTGATTCCAACCTCCGATTCAAGAGATGAAGTGAATGAATTTTGTG
 AGAAAGAGGGCTTTAAATAAAGCAAAACAAAGCAATGCTTGCAAAACTCATGTCTGAATTA
 GAAAGCTTCCCTGGCTCGTTCCGTGGAAGACATCCCTCCCAAGGCTCCGACTCACAATCAAGG
 AGACCCGGAAGGCGTACATTCGCCGGGTGTGCTTCCAGGAGAAACCTGGAACGAGAGCTCG
 TCCTCTTACCAAGGTCAAGGTCCCGGATCTCGGGTCCCTTGACGCTCTACCCATGGAGGAGGA
 GGAGGAAGAGGATAAGTACATGTTGGTGAGAAAGAGGAAGACCGTGGATGGCTACATGAAT
 GAAAGATGACCTGCCAGAAACCCGTGCTNCAATCAATCCGTGACCTTCCGCATATAATTCCG
 CCAAGTGGAGAAATACAGAAAGGAGGAGTGGAGAAACGCTGACGCAATTCGGAAGAGA
 AGATTATAACCGTTCACTGGGTTCTACTTGTTCATCAATGCGCTCAGAACTATTGATACCAA
 AACAACTGCGAGAAACCAAGACTGCTGGGCGCTTCAAGGCCAGTCTGTGGCCCTGCCTCG
 AAACCGTTATGGTGAAGAGGTCAAGGATGCTGTGCTGGATCCGAACCTGGCATTCGCCCGCTTG
 TCGAGGAATCTGCAACTGCACTTCTGCCGGCAGCGAGATGGACGGTGTGCGACTGGGGTCT
 TGTGTATTCCCAAAATATCATGGCTTTGGGAATGTGCATGCCACTTCTGAAAGCTGAAACA
 GGAATTTGAAATGCAAGCATAATATCTGGAAAAATTTGCTGCTGCTTCTACTTCTCAAAATCTT
 TCTTGTAAAAAGTTTCCAATTTTTTCACTGAAACCTGAGTTAAAAATCTTGATGATCAGCGCTGT
 TATATGAAAGAACTCCAATCAAGTIACTTACGAGCATGTGTTCTGGAGCATCACAGAAAGG
 TATATTGCTAGTTACACTTTGCCCTCTGCACTTCTCTGCTGCCACCCCTCACTCATAGC
 ATTCGCCCTCTATTTCCTATGCTCCCTCTCCCAACCCCTTAAAGTTTCTGAAATTTCTTTTAA
 AAWTTACAGTTTTAAGGAAAAGCCATATTTTAACTACCTGGGTGTGGAAATAGCCCTTCCAT
 AAAACCCCTAAGCACTTGGAAACACAAATATAGTATTAACCTTAACCTAGATCCATTTGAATTTCA
 GAGAAGAGCCCTCTAACTGTGTTTACACAAAAACGAGTATGATTTAGCATTCATAGTTTGA
 ATTTTTAAATAGAAATCAAGGCACAAAAGTCTTAAACCCATGGGAAATAGGTAATTATKGC
 ARATTGAGGGTCTCYCAATCCCAAGWATKGGCTTATGKTACMARKKGGTGTGCMCAGTTAG
 ACYTAATTTCTCTAATTTCTCTGCGGGAAGGKWAAGKGGCGCTGCTACMCGATCAT
 AATTCAAGGKGTGGKGGSCAATGTAAATTTAATTAATTAATTAATTTAGTATGATTTGCAAA
 AGATTATWAGATTAAGCTGATTTGAATTTTCAGTATAAAACCTTAGTATAATTTGATTTGCAAA
 GKTATTTTCACTTACATGTAAAGGKATTTGCAATAAAATCTTGGCAAAATTTGKATTTGGAACCT
 TGATATTAAAACTAGTCTGTGGKCTTTGCACTTCTTGTAAATTTATAAAACGAGGCAAAAG
 TCTCAAGTTTATGATTTTAAAGCACTTTATAAACAATGATAAGTGCCTTTTGGAGATGTAACCTT
 TAGCAATTTGTTAACTGACATCTCTGCCAGTCTAGTTTCTGGGCAAGTTTCTGCTGTGTCAGTAT
 TCCCCCTCTCTTTGCAATTAACAGGATTTGGTAGAGGTGGAATCTAAGTGTGTTGATGTC
 CAATTTACTTGCATATGTAAACCAATTTGCTGTGCCATTCATAGTTTGAATGCAATTTGGAC
 CTTGAATCTGATAAGTGTAAATACAGCTTTTGTCTGTAATGCTTTTATACAAAGTTTATT
 TTAATTAATAAAATGTTTGTCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
 CCCTTGTGAGKSWTAAATTTAGCTTGGCACTGGCCGTCTGTTTACAACGCTGTGATGGGA
 AAACCTGGCGTTACCAACTTAAATGCGCTTGCAGCACAATCCCTCTTTCGCAAGCTGCGGTAA
 TAGCGAAGAGGCCCGCAACOGATGCGCTTCCCAACAGTTGCGCAGCTGAAATGGCGAATGGG
 AGCGGCCCTGTAGCGGCGCATTAAGCGCGCGGGTGTGGTGGTTACGCGCAGCGGTGACCGCTA
 CACTTGGCAGCGCCCTAGCGCCGCTTCTTTCCGTTCTCTCTCTCTGCGMCGTTTCCGCGG
 CTTTCCCKCAAGCTNTAAATCGGGGG

One position equals 20 bases

- if more than 2 bases disagree with consensus sequences
- if more than 10 positions are unknown
- if more than 10 positions are gap characters

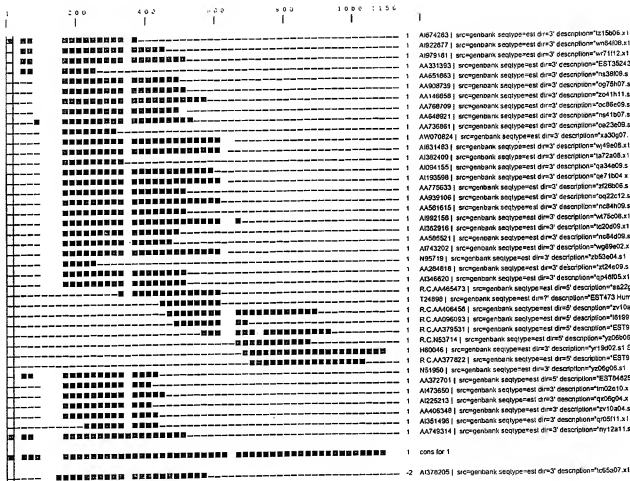


FIGURE 28A

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METSESSSDS CDSFASDNFA NTRLQSVREG CRTRSQCRHS GELRVAMKFF
ARSTRGATNK KAESRQPSFN SVTDSNSDSE DESGMNFEK RALNIKONKA
MLAALMSELE SPFGSFRGRH PLPGSDSQSR RPRRRTPEGV ASRRNPERRA
RPLTRGRSRI LGSLDALPME EEEEEOKYML VRKRKTVDGY MNEDDLPRTR
RYRSSVTLPH IIRPVEIQK ERSWRTSAAI LEEKIITVHW ALLVINAVRR
LLIPKOTAEI QTAGAFEASS VAPAFETVMV KRSCMLCWIR TGIARLVEES
ATAVSAGSEM EGVRLGSLCI

FIGURE 29

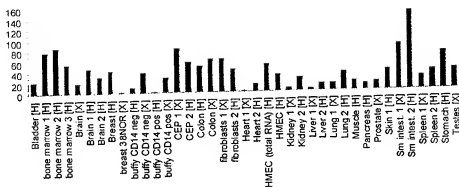


FIGURE 30A

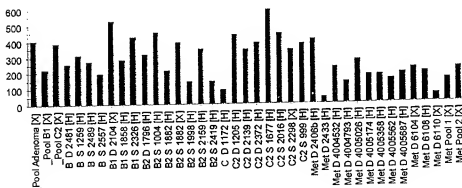


FIGURE 30B

ACTCACTATNGGGCGAATGGGCCCTCTNNATGCATGCTCGAGCGCCCGCCAGCTGTGATGGATA
TCTGCAGAAATTCGCCCTTAAGCAGTGGTAACAACGCAGAGTACCGGGGGGAGACCGGAGGG
CAGAAGGCAGAGTCCAGGCTTAGACTGCAGTTCCTCGCTTACCTGTGCAGTCTAATTTTGAGC
TGCCTCTTGTAGTCTTAAAGGACAGGAGCTTCGTGTGTGGGTCTGTCTAAACCCGTACGTTTCC
GTGGGCAAGTCGTGTACTCCTGGCGCTGCTCAGCTCCAACACGCTTCTACACTGATAAC
AAGAAATATGCCGTAGATGATGTTCCCTTCTCAATCCCTGCTGCCTCTGAAATTCGCCACCTTA
GTAACTCATCAATAAACTACTAAAGGACAAAATAGATTCCACAAAATCATGTGGAGTTTGATT
TCCTTATTAAGGGCCAGTTTCTGCGAATGCCCTTGGACAAACACATGGAAAATGGAGAACATCT
CATCAGAAAGAGTTGTGGAAAATAGAAATACGTTGGAGAAATATACCTGCACCCACGCCAGAGCAA
TGCAATGTTCCATGATGACTGGATCAGTTCAAATTAAGGGGCGAGGAAATGGAATCTTGACTGGT
TCCTATGATAAGACTTCTCGGATCTGGTCCTTGGAAAGGAAGTCAATATGCAATTTGTGGGA
CATACGGATGTTGTAAGAGATGTGGCCTGGGTGAAAAAGATAGTTTGTCTCTCTTATTATTG
AGTGTCTTATGGATCAGACTATTCTTATGGGAGTGGAAATGTAGAGAGAAACAAAGTGAA
AGCCCTACACTGCTGTAGAGGTCAATGCTGGAAAGTGTAGATTCTATAGCTGTTGATGCTCAGG
AACTAAATTTTGCAGTGGCTCCTGGGATAAGATGCTAAAGATCTGGTCTACAGTCCCTACAGA
TGAAAGAGATGAAATGGAGGAGTCCCAAAATCGACCAAGAAAGAAACAGAAAGACAGAAACAG
TTGGGACTACAAGGACTCCCATAGTGAACCTCTCTGGCCACATGGAGGCGAGTTTCTCAGTT
CTGTGGTCAGATGCTGAAGAAATCTGCAATGCATCTTGGGACCATACAATTAGAGTGTGGGTT
GTTGAGTCTGGCAGTCTTAAGTCAACTTTGACAGGAAAAAAGTGTTTAAATTTGATTTCTCTATT
CTCCACTTTGTAAACGTTTAGCATCTGGAAGCACAGATAGGCATATCAGAGCTGTGGGATCCCG
GAACTAAAGATGGTCTCTTTGGTGTGCGCTGTCCCTAACGTCACATACTGGTTGGGTGACATCAG
TAAATTTGGTCTCCTACCCATGAACAGCAGCTGATTTCAGGATCTTTAGATAACATTTGTAAGC
TGTGGGATACAAGAGTTGTAAGGCTCCTCTCTATGATCTGGCTGCTCATGAAGACAAAGTTT
TGAGTGTAGACTGGACAGACACAGGGCTACTTCTGAGTGGAGGAGCAGACAAATAATTTGTAT
TCCTACAGATATCACTACCACTTCCCATGTTGGGGCACTAAGTGAACAAATAATTTGACTA
TAGAGATTATTTCTGTAAA-TGAAAATTTGATAGAGAACCATGAAATTAATCATAGATGCAGATGCA
GAAAGCAGCCTTTTGAAGTTTATAATGTTTTCACCTTCATAACAGCTAACGTATCACTTT
TTCTTATTTTGTATTTATAATAAGATAGGTTTGTGTTTATAAAATACAACTGTGGCATACA
TTCTCTATACAACTTGAATTAACCTGAGTTTACATTCTCTTTAAARGTAAAAAAA
AAAAA

FIGURE 31

One position equals 17 bases.

■ if more than 1 bases disagree with consensus sequences.

- if more than 8 positions are unknown.

_ if more than 8 positions are gap characters

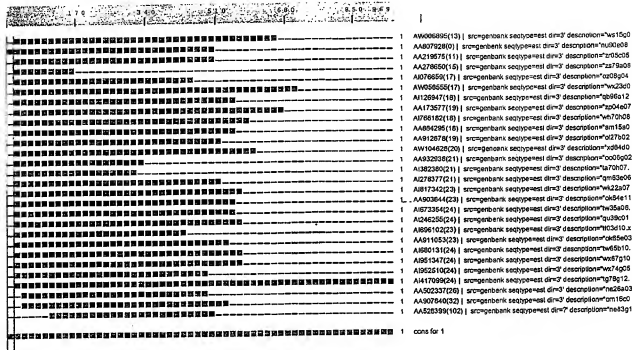


FIGURE 32A

[illegible]

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FIGURE 32B

MAQLQTRFYTDNKKYAVDDVPFSIPAASEIADLSNIINKLLKDKNEFKHVEFDF
 LKGGQLRMLPLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSKGA
 EEWILTGSYDKTSRIWSLEGKSMITIVGHTDVVKDVAWVKKDSLCLLSASMD
 QTILLWENVERNKVKAHCCRGHAGSVDSIAVDGSGTKFCSGSWDKMLKIWS
 TVPTDEEDEMEESTNRPKKQKTEQLGLTRTPIVTLSGHMEA VSSVLWSDAEEIC
 SASWDHTIRVWVVESGLKSTLTGNKVFCISYSPCKRLASGSDRHIRLWDPR
 TKDGSLSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDTRSCKAPLYDL
 AAHEDKVLSDWTDTGLLSGGADNKLYSYRYSPTTSHVGA.

FIGURE 33

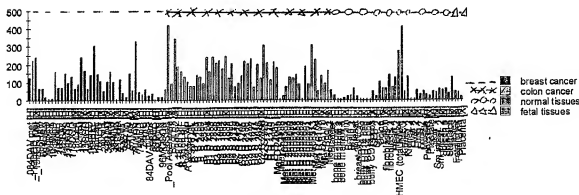


FIGURE 34

AGAATGGCTGGGCTCCITTCGCCGCCGGTATTCCTGGTATATGATCCCACTCTCACTCTCATAGGAGAC
 GATCTCGAAGTAGATCATATACCCAGAAATACCGGCCGCGAAGGAGCCGAAGCTCAAGGGTAAGACAGTA
 GAAATATTATTCAGTAACCAATAATGTGTGAACCTTTANGATGGATAATAGGGCATGGACTGAGTGCTGCT
 ATCTTGAAATGTGCACAGGTACACTTACCTTTTTTTTTTTTTTTTAAAGTTTTCCCATTCAGGATAACA
 ACATTGTGATCTGTACTACAGGAACCAATGTCTATGCGCTGTACATGTGGCTATAAAGTACATTAATATA
 TCTAATCTATTCATAATGTGGGTGGGTAACTACTGTCTGTGAAATAMGTAGAGAGCTTTCACTTAAAAAA
 AATGCAITTACTTTCACTTAAACACTAGACACCCAGGTCCAAJAATTTTCAAGGTTATAGTACTATTTTCAACAA
 TTCTTTAGAGATGCTAGCTAGTGTTCAGACTAAATAATAGCTTTATTTATGTGAATTTGTGATTTTTTATGC
 CAATAATTTTTAGTTCAATCATTTGATGATAGCTTGGJAATTAATAATATGCCATGGCATTGACATTT
 GATTAATCCATAGAGATCAAAATGAGTTTACAGAGAACTGGTGGTTGAGCTGATTATTAACAGTTACTG
 AATTCATTTTATTTTCTTACATTATCCATTGTATTTAGGTTTCTCTTTACATTCTTTTATATGCA
 TTCTGACATTACATATTTTAAAGACTATGGAATTAATTTAAAGATTAAAGCTCTGGTGGATGATATCTG
 CTAAAGTAGCTGAAATGTAAATTTTGTAACTGTAAATATACCTGTACACAAATGCTTTTCTAATG
 TTTAAACCTTGAGATTCCAGTTGCTGCTTTGTACAGAGGTTACTGCATAAAGGAAGTGGATTCAATAA
 CCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 39

FIGURE 40

CAGCGGCGCGCTGAATTTCTAGGGCGGGTTCGGGCCCGAAGGCTGAGAGCTGGGGCTGCTGTCGTGCGCTGTG
 TCGCCGACCGCGGAGCTCCGCGGCGGGACCCGCGGCGCCGCTTTCTGCCGACTGGAGTGTGCGGGAAG
 AAGCGCTTCTCGCCGCCAGAGATTTCTCTCGCGCGAAGGACAGCGAAAGATGAGGTTGGCAGGAAGA
 GAAAGCGCTTCTCTGTCGCGGGGTGCGAGCGGAGGGGAGTGCCTATGTTCTCTCCATCTAGTGTGGC
 CGTGTGCGCTGTGGCTGCACCTTGGCGCTGGGCGTGCGCGGCGCGCTCGAGGCGGGTGGCGATCCCTATG
 TCCCGGACATGCCCTGGAACATCACGCGGATGCCCAACCACTGCACCACAGCACGAGGAGAACGCCA
 TCTGCGCCATCGAGCAGTACGAGGAGCTGCTGGACGTGAACGTGCAGCGCGCTGCTGCGCTTCTTCTCTG
 TCCATGTATCGCGCCCATTTGACCCCTGGAGTTCCTGCACGACCCCTATCAGCGGTGGAAGTCTGGTGTG
 TGGCCTATCGAGCAGTACGAGGAGCTGCGAGCGCCCTCATGAAGATGTACAAACAGCTGGCCGAAAGCTGSCCT
 GAGCGACAGCTGCGCTGTCTAGCCCTGGCGTGTGCATTTGCGCTGAAGCCATGTCAGGAGCTCCCGGA
 GAGATGTTAAGTGSATAGACATCACACCAGACATGATGTTACAGGAAGGCGCTCTTGATGTGACTGTAA
 CGCTTAAGCCCGATCGGTGCAAGTGTAAAAAGGTGAAGCTAATTTGGCAAGTATCTCAGCAAAATCT
 ACAGCTATGTTATTCTATGCCAAATAAAAGCTGTGCAAGAGGAGTGGCTGCAATGAGGTCAACACGGTGGT
 GGAATGTAAAGAGATCTTCAAGTCTCATCACCCTACCCCTGCAACTCAAGTCCCGCTCATTAACAATTC
 TCTTGGCAGTGTCCACACATCTGCCCCATCAAGATGTTTCATCATGTTTACGAGTGGCGTCAAGGA
 TGAATGTTCTTGAATTTGCTTAGTTGAAATGAGAGATCAGCTTAGTAAAGATCCATACAGTGGGA
 AGAGAGGCTGCAAGAACAGCGGAGAACAGTTCAAGACAGAAAGAAACGCGCGCGCCACAGCTGTGAT
 ATCCCCCAGAACAAAGGGAAGCGCTCCTGCTCCCAACAGCGAGTCCCAAGAGCGGAGCTCCCGAC
 GAGTGTGCCAGAAAGAGAACAAACCCGAAAGAGTGTGAGCTTACTAGTTTCCAAAGCGGAGCTCCCGAC
 ACTCACTGCAAGTGTCTTCATAGACACATCTTGCAAGCTATTTTCTTAAGCGTATGCTTCAAGTTTTCTTT
 CTAAAGCCATCACAAGCCATAGTGGTAGGTTTGCCCTTTGGTACAGAGCTGAGTAAAGCTGGTGGAAAA
 GGCCTTATGCAATGCAATCAGAGTAACCTGTGTGCACTACTAGAGAGTGGGAAAAATAGCTGTGTA
 CAATTCGACCTTAATATGTGCAATGTAAATATAAGGCAATTTTCAAGAAACAGTAATTTTATACAG
 TATGTTTTTAAGAGGAACAGTAGTGAATGAATTTAAGAGTAGCATATGGAATATAATATGTTGTTTTT
 TACCAATGACTTCAGTTTTCTGTTTTAGCTAGAACTTTAAACAAATAATATAAAGAAATATAAT
 TTTTGTGATGAAGGGGATTTTTGAAATTTAGAGTAAGAACTTTAAACAAATAATATAAAGAAATATAAT
 TTAGCAACCCCTTTAAGCAGCACCAAGAACAGTGAATTTGTCTACCATAGGAGTAGGTACTAT
 TAGTTGGCTAATGCTCAAGTATTTAAGCTTAAATAGGCTTCAATGTGAGTGCAATTTTGTGTTCTCAT
 CCAACCTGAGAAATATTTAGCAAGCTTAAATAGGCTTCAATGTGAGTGCAATTTTGTGTTCTCAT
 TTAATATTTTTTTGCTAATACATGTGAGAGGAGTAAATATAATGTACAGAGAGGAAGTGTGAT
 TCCACCTGTAATGAGAACTTACTCAAGTTGGGACTTTAATCAGAAAAAGAACTTTATTTGGCAGC
 ATTTTCTCAACAAATTCATATTTGAGCAATTTGGAGCAATTTTAAAAACAATTTATTTGGCCT
 TTGTCTACCAAGTAAAGCTATCTCCACTACACAGAGGTAATCACTATTAGTATTTTGGCATATATCTCCAGGT
 GTTGTCTATAGCACTATAAATGATTTGAACAAATAAAGCTAGGAACCTGTATACATGTGTTTCTATAC
 CTGCGCTCCTTTCTGCGCCCTTATTGAGATAGTTTTCTGCTCAAGAAAGCAGAAACCTCTCATTTCT
 AACGCGTGTGTTATTCATATGATATGCACTACTCAACAACTGTGTGCTATTGGATAGCTTAGGTGTT
 TCTTCACTGACAACTAGTAATACATCTACCGGAATTC

FIGURE 41

SAITTAATCCTATGCAAACTAAGTTGGTCTGCTCCACCTGTTTGGTGAGGTTGTGTAAAGAGTTGT
 GTTGGCTCAGGAAGAGATTAAAGCATGCTGCTTACCCAGACTCAGAGAAGTCTCCCTGTTCTGTGCTAG
 CTATGTTCTCTGTTGTGTGCATTCTCTTTTACAGAGCAAAACGCCCCAGTAGAAGTGTGTAATGGGCGC
 ACGCTGCAGAGSATCCTGGCGGCTGTGAACAACACTCCACCAAGACTGGAAAGATCTGGCTCACCGTCC
 TCTTCATTTTTCGATTTATGATCTCGCTGTGTGGCTGCMAGGAGGTGTGGGGAGATGAGCAGGCCGACTT
 TGTCTGCAACACCTGCAGCTGATCTTCTGTGCCAGCCAGGCTCCTAGTGGCCATGCACTGGGCTTACC
 CGGCTATGGGCGCTGCAGAGCAAGTTCATCAAGGGGGAGATAAAGAGTGAAATTAAGGACATCGAGAGAT
 GGAGACATCGAGCAAGAGCAAGTTCATCAAGGGGGAGATAAAGAGTGAAATTAAGGACATCGAGAGAT
 CAJAJCCGAGAGCTCCGCATCGAAGCTCCCTGTGTGGTGGACCTACACAGCAGCATCTCTTCCGGGTCT
 ATCTTCCGAAGCCGCTTCAATGTACGCTTCTCATGTCTAGCAGGGCTTCCCATGCAAGCGGCTGGTGA
 AGTCCAGCCGCTGGCTTGTCCCAACACTGTGGACIGCTTGTGTCCCGGCCACGGAGAAGCTGTCTT
 CACAGCTGTCTATGATTGACGTGTCTGGAAATTGCACTCTGTCTGAATGTCTGAATTTGTGTATTGTCTA
 ATTAGATATTGTTCTGGGAAGTCANAAAAGCCAGTTTACCGCATTGCCAGTTGTTAGATTAAAGATAG
 ACAGCATGAGAGGGATGAGGCANCCGTGTCTGAGCTGTCAAGGCTCAGTCCGCAAGCATTTCCACACAA
 AGCTTCAGCCTTAAATGCAACATTGAAACCCCTGTAGGCTCAGGTGAACTCCAGATGCCAATG
 AGCTCTGCTCCCTTAAAGCTCAJAJAAGGCCCTAAATCTATGCTGTCTAAATTTCTTCACTTAAG
 TTAGTCTCACTGAGACCCAGGCTGTTAGGGGTTATTGGTGTAAAGTACTTTCATATTTAAACAGNGA
 TATCGGCTTTGTTCTTCTCTGAGGACAGAGAAJAJAGCCAGGTTCACAGAGGACACAGAGANGGT
 TTGGGCTGCTCTCTGGGGTCTTTTGGCACTTTCCCAAGTTAAAGGTGAACATTGGTCTTTTCATTT
 GCTTTGGAGTTTAAATCTCAACAGTGGCAAGGTACAGTGCTTAAACTCTGTATACACTTTTGGGA
 GCTGAAACTTTGTAGTATGATAGGTTATTTTGTATGATAAGATGTTCTGGATACCAATATATGTTCCGCC
 TGTTCAGAGGCTCAGATTGTAAATGTAAATGATGTCTATGCTACTATGATTTAATTTGAAATATG
 GCTTTTGGTTATGAATCTTTCAGCACAGCTGAGAGAGGCTGTCTGTTGATTCATTGTTGGTCTATAGC
 ACCTAACACATTGAGGCTCATCTGAGTGAGACAGACTAGAAGTCTCTAGTTGGCTTATGATAGCAAT
 GGCTCATGTCAAATATTAGATGTAAATTTGTGTAAAGAAATACAGACTGGATGTACCAACACTAC TACC
 TGTAAATGACAGGCTCTCCACACATCTCCCTTTCCATGCTGTGTGAGCCAGCATCGGAAGAACGCTG
 ATTTAAAGAGGTGAGCTTGGGAATTTATTGACACAGTACCAATTTAATGGGGAGACAJAJAATGGGGCCA
 GGGGAGGGAGAGTTCTGTCTGT/AAAAAGAGTTTGGAAAGACTGGACTCAJAJAATCTGTGATTAAAG
 ATGACCTTTGTCTACCTTCAAAGATTGTTTGGCTTACGCCCTCAGGCTCCAATTTTAAAGTGAAT
 ATAACTAATAACATGTGAAGAAGATAGAAGCTAAGGTTTAGATTAATATTGAGCAGATCTATGGAAGAT
 TGAACCTGAATATTGCCATTATGCTGTGACATGGTTTCCAAJAJAATGTACTCCACATACTCTAGTGGG
 TAGATATTTTCTGTGTCAAGATAGCATGTAAAGCATTTTGTAAATAAAGAAATAGCTTTATGGA
 TAGTGCTGTAACTAAAAAATTTTGTAAATGATCAATACATTTAAACATTAATAATAATCTCTATAJ

T

FIGURE 42

CGGCCAGCACACCCGGGCACTCCTCTGCGGCAGCTGGGCGCTCGCAAGCGCAGTGCOCGACGCGACGCCG
 GAGTGGCTGTAGCTGCTCGCGCGGGCTGCCGCCCTCGCGGGCTGTGGGCTGCGGGCTGCGGCCCGCGCT
 GCTGGCCAGCTCTCGACGCTCGCGGGCTCTGCGGGCGCCGCTGCTCTGCACGCTGCGGGCGGGCATG
 GGAATACGCGGCCAATGCTGCGCGCAGATCGCTCTCGCAGGATGAGGGAGTGTGGGTCCAGGTGGGGCTG
 CTGGCCCTGCCCCCTGCTTGCCTGCGTACCTGCACATCCACCCCTCAGCTCTCCCTGCCCCCTCACTCAT
 CTGAAGTCTTCAGGCAAGTAGTTGTGCTTTTACACGGTITTCACACATCCAGCTACGACTGGTACAGATTGG
 TGGAACTCCAGAGATAGTTGTGCTTTTACACGGTITTCACACATCCAGCTACGACTGGTACAGATTGG
 AAGGCTCTGACCTTGAGGTTTCATCGGGTGATTGCCCTTGATTTCITAGGCTTTGGCTTCAGTGACAAAC
 CGAGACCACTCATATTCCATATTTGACGACGGCCAGCATCGTGGAAACGCTTTTGGCGCATCTGGGGCT
 CCGAGACCACTCATATTCCATATTTGACGACGGCCAGCATCGTGGAAACGCTTTTGGCGCATCTGGGGCT
 TACAGACCGCAATCCAGCTTCTTCTCATGACTATGGAGATATTGTGCTCAGGAGCTTCTCTACAGG
 TACAGACCGCAATCCAGCTTCTTCTCATGACTATGGAGATATTGTGCTCAGGAGCTTCTCTACAGG
 AGACTCCAGCTTCCAGCTTCTTCCAAAGCTACTCAAGATGGAGGTGTGCTGTCAACCATCTCTACAG
 ACTGATGAATCTTTGTATTCTCTCGAGGTCTCACCCTCAGCTTTTGGGCCGTATACTCGGCCCTCTGAG
 AGTGAGCTGTGGACATGTGGCCAGGGATCCGCAACATGACGGAACTTAGTCATTGACAGCTCTCTTAC
 AGTACATCAATCAGAGGAAGAGTTTACAGAGGCGCTGGGTGGGAGCTTTGGCTCTGTAACTATCCCAT
 TGAATTTATCTATGGGCCATTGGATCTCTAAATCCCTATCCAGAGTTTTTGGAGCTGTACAGGAAACG
 CTGCGCGGCTCACAGTGTGATTTCTGGATGACCACATAGCCACTATCCACAGCTAGAGGATCCCATGG
 GCTTCTTGATGCATATATGGGCTTCACTCACTCCTTCTGAGCTGGAAGAGTAGCTTCCCTGTATTAGC
 TCCCTTACTCCCTATATGTGTGTGATTTCCACTTAGGAAGAAATGCCAAAGAGGCTCCTGGCCATCAA
 CAATTTCTCTCACAAAGTCCACTTTACTCAATTTGGTGAACAGTGTATAGGAAAGGCGCAGCAGGAGCT
 CTGACTAAGGTTGACATTAATAGTCCACTCCCATTACTTTGATATCTGATCAAAATGTATAGACTTTGGCT
 TGTTTTTGTGCTATTAGGAATTTCTGATGAGCACTACTATCCAGTATGACAGAAAGAGCTTTCTTTGCA
 TAAAGCAATTTTTTAACTTTTGGACTTCTCTGAATATTTTGAAGTGCTAATTTCTGGCCCAACCC
 AACAGGAATTTCTATAGTAAGGAGGAGGAGAAAGGGGGGCTCCTTCCCTCTCTCGAATGAGCTTTTGGCA
 CATGCCCTTTAAAGTTCTTTAAGCAACACAGAGCTGAGTCCCTTTTGTATACCTTTGATCTTGTAGTGT
 TCACTAGCTGTTTTTAGTTATTAACATTTTGTTAATATAGATATTGGTTAAATGATACGATTTTAGG
 TATGATTTAAGACTATGATTTACCTATACATATATATATTTTATAAGATACTAACCAAGCACTACCTT
 ACTCTGCCAGAGTAGTGAAGCTAATTAACACGTTTGGTTTCTGAATAAATGACTAATCCAACTAT
 TTCTCAAAATCACAGGACATTAAAGACCAATAGCATCTGTGCCAGAGATGATCTGTTTAGCTGGGAG
 ACCAATTTCAACAGCAATTAACAGCTGAGACTCCTCATACCTCAGTGGTTAGAGGCTTCTCTTTTGA
 GCTACAGTAGAGGGGAGGGGATTGTGTGTAGTCAAGTCACCACTGTGAATGATACACTGATTCCTTTATG
 NTAAGTCTTTACTCCCCACTGCGTGTCCAGAGAGGCTTTCCATGTAGCTCAGTAATCTCTGTACTT
 TACAGACAGGAAAGTCCAGAAACTTTAAGACAAACTCTGAAGACCTTAGAGCAAAATGGTGTGAATA
 CTTTTTTTTTAAAGCCACATTTTCACTGTCTAGTCAAGCGGATTTAAGTGTATTTTAAATTCGT
 TTTTTTAAATTAGCAACTTCAAGTATAACAACCTTGAATCTGGAATAGTGTATTTTCTATTAATAA
 AATGATTTGTGACAAAATAAACCG

FIGURE 43

CTCTCAGTGTCCAGTGGTCASTTGCCCCAGGATGGGGACCCACAGCCAGAGCAGCCTTGGTCTTGACCTAT
 TTGGCTGTGTCTCTGCTGCTCTGAGGGAGGCTTCAGGCTACAGGACAGAGGAGCTGAGGCGCAGAGC
 ACTTTCAAGAGTTGGCTACGAGCTCCCCCTCCCAACCCCTATCCGAGGCCCTCCCATGATCACC
 TGACTCTCTCAGCATGGCCCTCCCTTTGAGGGACAGGTCAAGTGCAGCCCCCTCCCTCTCAGGAGGCC
 ACCCTCTCCACAGGAAAGCTGCTACTCTGCCACTCCCTGCTGMAAGGAGTGGGTCCCCCTCTCC
 CTCAGGAAGCTGTCCCCCTCCAAAAGAGCTGCCCTCTCTCCAGCACCCCAATGAACGAAAGGAAGAAC
 GGCACCTCCATTGGGGACACAGCCATCCAGAACCTGAGTCTCGAATGCAGCCACACACTGCCAACAG
 SAGCGGTCCCAAGGSGGCTGGGGCCACCGGCTGGATGGCTTCCCCCTGGGCGGCTTCTCCAGACATC
 TGAACCAATCTGCCTTCTTAACCTGACAGCATGTGATATATGGTCCCTGGAACTACCAAGTCCAGCTA
 CTCACACTCACTCGCCAGGTGAGACCTCAATTTCTGGAGATTGGATATTCCTGCTGCTGCCACTGCG
 CGCAGCCACACAAACCGCTAGAGTGTGCCAACTTGTGTGGGAGGAAGCAATGAGCGATTCTGTGAGG
 CCGAGTTCTCGGTCAAGACCCGACCCCACTGGTGTGCACGCGCCAGGGGAGGCTCGGTTCTCTGTCT
 CCAGGAGGAAGTCCCCAGCCACACTACAGCTCCGGGCTGCCCGAGCCATCAGCTGTATTTCTCG
 GGTCTTGAGCTCCCTTTCCCTCTCGGGGTGCCACATTGACAAATATCAAGAACATCTGCCACTGAGGC
 CCTTCCGCTCTGTGCCACGCAACTGCCAGCTACTGACCCCTACAAAGGAGGCTGCTGGCACTGATCCA
 GCTGGAGAGGGAGTTCCAGCGCTGTGCCGCCAGGGGACAAATCACACCTGTACATGGAGGCTGGGAG
 GATACCTTGACAAATACTGTGACCGGGAGTATGCTGTGAAGACCCACCACTTGTTGTTGCCGCGACC
 CTCCAGCCCTACTCGGATGAGTGCTTTGCCCGTGGGCTCCTTACCCCACTATGACCGGGACATCTT
 GACCATTGACATCAGTCGAGTCACCCCAACCCTCATGGGCCACTCTGTGGAACCAAGAGTTCTCACC
 AAGCATAAACATATTCTGGGCTGATCCACACATGACTGCCGCTGTGTGACCTGCCATTTCCAGAAC
 AGGCTGCTGTGCAAGGAGGAGAAATTAACCTTCATCAATGATCTGTGTGGTCCCCGAGCTAACATCTG
 GCGAGGCCCTGCCCTGTGTGTACTGAGTCTGGGGATGAACAGGTCAACTGCTTCAACTCAATTTAT
 CTGAGGACGTGGCTCTAGTGTCTGGAGACACTGAGAACGCCAAGGGCCAGGGGAGCAGGCTCACTG
 GAGGAACAAATATCAGCTCCACTCTGAGCCCAAGGAAGAAATGCTCACCCAGAGCCCTAGAGGGTCA
 ATG

FIGURE 44

ACTCACTATATAGGGCTCGA3CGGGCCGCCGGGAGG1GGCCACCCACCATCATCTAAAGAGATAAACTTGG
 CAAATGACATCGAGGTTCTTCAGGCGAATAATTCGCAAAATCTTCAAAGGACCTTATCTGCAAGTGT
 CTGAAATACCTTTCAGATAGAGATGATTAATTCACACAGGATACCTAATCAAGMCTCCAGAAATCAGGA
 GACGGAGACATTTGTACAGTTTTCGACATTTGGACAAATACAAAGATATCTTGGTGTGCTCTGGTTT
 TGGCTGTCTCTGGGACAGAAATGCTGGGAGGCTCTGCTGAGCTCGAGATCCCGAGGTTCAAGAGCGG
 ATACAGGACGGACGAAACATCCGACCCAACTATTCTTGTGCTTACCGATGATCAAGATGTGGAGCT
 TGGGTCTCCGTCGACGCTATGACAAACGAGAAAGATATGGAACATGGGGGGGCCACTCTCATCTATGCTT
 TGTGATCTACACCATATGCTGCCGTCACGAGTCTCCATGCTCACCGGGAAGTATGTGCACAAACACAA
 GTCTACACCAACAGCGAGNCTGCTCTTCCGCTCGTGGCAGGCAATGCATGAGCTCGGATCTTGTGCTGT
 ATATCTTAACACACTGGCTACAGAACAGGCTTTTTTGGAAATACCTCAATGAATATAATGGCAGTCA
 TCCCTCCGCTGGCGCAATGGCTGGATTAACAGAAATCTCGCTCTATTAATACAGTTTGTGCGC
 ATATGCCATCAAGAAACGATGGATTAATGCAAGGACTCTTACAGACTTAATCACTAACGAGAG
 CATTAATTAATCTCAAAATGCTCAAGGAATGATCCCATAGGCCGTTATGATGGTGATCAGCCACGCTG
 CGCCCAAGCGGCCGAGGACTCAGGCCACAGTTTCTAAAGTGTACCCGATGCTTCCACACATAAAT
 CCTACTTAATACATGCAACCAATATGGATAAACACTGGATTATGAGTACACAGGACCAATGTGCCCCAT
 CCACATGGAATTTACAAUATCTACAGCGCAAGGCTCCAGACTTTGATGTCAGTGGATGATTTCTGTGG
 AGAGGCTGATTAATCATGCTCGTGGAGCGGGGAGCTGGAGAACTACTACATCATTACACCGCCGACCAT
 GTTATACCATATTTGGCGAGTTTGGATGCTCAAGGGGAAATCCATGCCATAGACTTTGATATTTCTGTGCG
 TTTTTTATTCTGGTCCAGAGTGAAGACAGGATCAATAGTCCACAGATCGTTCTCAAGTATGACTTGG
 CCCCCACGATCTGGATTAATGCTGGGCTGACACACCTCCTGATGTGGACGCAAGTCTGCTCCAACTT
 CTGAGCCAGTCAAGAGCGAGTAAACAGGTTTCGAAACCAAGAGGCGCAAAATTTGGCGTGAATCACTTCT
 ATGAGTGAAGAGCAAAATTTCTACGTAAGAGGAGAAATCCAGCAAGATATCCACAGTCAAACTACTGCG
 CCAATATTAAGCGGGTCAAGAACTATGCCAGCGGCCAGTACCAAGACGCTGTGACACAAACCGGGGCG
 AAGTGGCAATGCATGAGGATACATCTGCGAGCTTCGAATTCACAAGTGAAGAGACCCATGACGCTGT
 CACAGTCCGCGACGACCGCGAACCTCTACGCTCGCGGCTTCCATGACAAAGACAAAGAGTGCATTTGTA
 GGGAGTCTGGTTACCTGCCAGCAGAGCCAAAGAAAGTCAACGGCAATCTTGAGAAAGCAGGGGACT
 CCAANGTCAAGGCCAGATTTGCTCCATCTCCGACAGACGTTCTCTGTCCGTCGAATTTGAAGGTGAAT
 ATATGACATAAATCTGGAAGAGAGAGAAATGCAAGTGTGCAACCAAGAAACATTTGCTAAGGCTCATG
 ATGAAGGCCCAAGGGGCAAGAGATCTCCAGGCTTCCAGTGTGGCAACAGGGGCGAGTCTGCGCAGAT
 AGCAGCACCGCGTGGGCCCACTACCATGCTCCGAGTGACACCAAGTGTTTATTCTCCCATTAAGCTC
 TATCCATTGTGAGAGAGAACTGTACCAATGGGCCAGAGGCTGGAAGGCCATTAAGGCATCAATTGACAAAG
 AGATTGAAGCTCTGCAAGATAAATTAAGAAATTAAGAGAGTGAAGAGACATCTGAAGAGAGAGAGCTT
 GAGGATGTAGCTGCAATTAACAAAGCTATTACAATAAGAGAAAGGTTGAAGAGCAAGAGAAATTAAG
 GAGCCATCTTACCCATTCAGGAGGCTGCTCAGGAGTAGATAGCAAACTGCACTTTCTGAGGAGACAA
 ACCGTGAGAGGAGAGAGGAGAGGAGAGAGAGAGAGCGGACAGGAGAGGGGAGAGTGCAGGCTGCTGCG
 CTCATCTGCTCTCAGCATGACAAACCACTGGCAGACAGCCCGCTCTGGAACCTGGGATCTTCTGTGCT
 TGTGACAGTGTCAACAAATAACACCTACTTGTGCTGTGCTGACAGTAAAGAGCGCTAATTTCTTCTT
 GTGAGTTTGTGACTGGCTTTTGGAGTATTTTGATATGAATACAGATCCTTATCAGTCAACAAATACAGT
 CACACGGTGAAGCGAGGCTTTTGAATCAGTACACGTAACCTTGAAGTAAAGTGGAGGCTGTGACAGTGA
 TAAAGCAGTGAACCCAGAGCTTAAGAACTTGTGATTAAGTATGAGAGAGCTGTGACAGGATGTGACAGT
 GAGGAGTATGAGGATGATGGGAGGCTTATGAGTACAGCAAACTACAGACTAGTCTGGTGGAGCT
 AGAGGAGCTACACAGTGTGAAATGAAGAACTATGAGTACAGCAAACTACAGACTAGTCTGGTGGAGCT
 GAGCTATATCTGTGAGAGTGTGATAGATATTGACATCTGAGAGTACATATGAGCAAAATTAAGCA
 AATAGAGCTCAAACTCTCAAGGTACGGGCTCTTGGTCTCTCTGTGAGCAGCTGTGCTCATAGGAGAA
 GCGCTCTGCTGACTCAGATGAAGCCCAAGGCAATAGGTTGGGAAACACCTCAATTGACCTGCGACGCTG
 ACTTTCAGGCTGCAATTTGGAACCGACCAACTATAGTCCAGAGTAACTGAATGGAAATACCAAT
 CCAAGATTTAATCAATGAATCTGAAACACTGGAGAAACCGGAAATGAGCGGGCTGAGAGACATTA
 TCATCTGGAACCAATTTCAAGTGGATGGCATGACAGACTAGAGCTCGGGCCAGCCGAGCTGACG
 CATCTCGCAGGACCCGAAAGAACTCTCCCAATGATGCTGCTGGAAGGAACTTTTGTAGATCAAGTA
 TATCTCTGCTGCTATCCGATGGAATTTCAAGTCTATCAGATGTCACTAGCCACCGGAGAACCGAG
 TAAATCTCCAGCAATAGCGGGGAGATGTTGACCAAGGTGGAGAGAAATCAGCAAGAGGAGAGTACAGCACC
 TAGAGAGAGCGGCTCTCTCTCACTCTCTCTGATTAGATGAACCTGTTACTCTACCTAACACAGATTA
 TCTTTTAACTTTTATTTGTAAGTATTAATAGGTAATCAGAGCCACCAACTTCCAGGCTACCTGCTG
 ACCTTTGTGCGATGAAGCTAGGAGCATCTGAGCATGAGCAGCGCTGTGACACGAGACTCTCTGTTATATTT
 ACTATCTGCAAGAGTGAAGAAAGGCTGGGATATTTGGGTGGCTGTTGTTGATTTTGTCTGTTT
 TGTGTTTGTGATCAAAACAGTATTATCTTTGAAATGTCGAGGACATAAGTATATGATTTATCCAAAT

FIGURE 45A

CAAAGTAGGCTAGAATGGGCGCTTTCAGAGTGTCTAAACTTGACACCCCTGGTAAATCTTCAACACACTT
 CCAGTGGCTGGGTAATGAAGTTTGGATTCATTTTAAACCACTGGAAATTTTCAATGCCGTCATTTTCAGTT
 AGATGATTTTGCACITTTGAGATTAAATGCCATGTCTATTTGATTAGTCTTATTTTTTATTTTTACAGGC
 TTATCAGTCTCAGCTGTGGCTGTCTATGTGCAGAAAGTCMAATAAACCCCAAGGACGACACAGATAGGA
 TCACATATTGTTTGACATTAAGCTTTTGCAGAAATGTGCATGTGTTTTACCTCGACTTCCTAAATCG
 ATTAGCAGAAAGGCAATGGCTAATAATGTTGGTGGTGAATAAATAAATAAGTAACAAAWRAARAWNGC
 CTGCTCTCTCTGTGGCTAGCCTCAAAGCGTTTCATCATACATCATACCTTTAAGATTGCTATATTTGGGTT
 ATTTCTCTGACAGGAGAAAGATCTAANGACTTTTATTTTCATCTTTTTTGGTTTTCTTGGCATGACTA
 AGAAGCTTAATGTTGATAAATATGACTAGTTTGGATTTACACCARGAAGCTCTCAATAAAGAAAAATC
 ATGAGTGTCTCCCAATTTCAACATACCCCAAGAGAACTAATTTCTTAACATTTGTGTTCTATGATATTTG
 TAAGACCTTCACCAAGTTCGTATATCTTTTAAAGACATAGTTCAAAATTGCTTTTGAAATCTGTATTCTT
 GAAATATCTTGTGTGTATTAAGTTTAAATACCAAGCTAAAGGATTACCTCACTGAGTCATCAGTACC
 CTCCTATTGAGTCCCAAGATGATGTGTTTTGCTTACCCTAAGAGAGGTTTTCTCTTATTTTAGATA
 ATCAAGTGCTTAGATAAATTATGTTTTCTTTAAGTGTATAGGTAACCTTTTAAAGAAAAATTAATAT
 GTTATAGCTGAATCTTTTGGTAACCTTAATCTTTATCATAGACTCTGTACATATGTTCAATTAGCTGC
 TTGCTGATGTGTATCATCGGTGGATGACAGAACAAACATATTTATGATCATGAATATGATGCTTTGT
 AAAAAAGATTCAAGTATTAGGAAGCATACTCTGTTTTTATCATGTATAATATTCATGATATCTTTAT
 AGAACAAATCTGCGCTTCAGGAAGCTCTAGAACCAATATTTCTCAATAAAGGTGTTTAACTTTAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 45B

CAAGAATTCCGGACGAGGGCGTGTCCAGAAAGTGGTACTGTGCTAGTATTAATCTCAGCTGGCAGGT
 TCCCTGAGTGCAGCTGGCTCGATAGTCGTAATGAAGAGTGTGCCGAAAGACTTTGAATCCAGATGAA
 TGTAGTACAGGAATTAATATTAAGTCTAGGATCAGAGGGAGCTGAGAGCTGGGCTCCTCTAGATTTCAAA
 TCAATATTAAATATTATCCACCACCTCAAGAGGAGCTTTGGTGGCAGCCCAAGATTTTTCTGTGCCCGGC
 TGTGGAATCCAGTAGAGCCTAAGTTTGTGAGCGGGCTCCGGTACTGCGAATACCTAGGGAAGTATTTCTG
 TGACTGTCTCCACTCATATGCAAGAGTCGTGCATCCCTGCCCGAATCTGATGATGTGGGACTTCAAGAAGT
 ACTACGTCAAGCAATTTCTCCAAACAGCTGTCTGCAGCAGCATATGSCACAGCCCATTTCAATTTGCTGAGC
 ATCGGCCAAGGCTGTATGCGAAAGGCCAAGAGCTGAGACAGAGTGAAGGAATTCAGGAGCAGCTCTTCCA
 ATCAAGAGAGCTGTTGAAGACCTGTAGGTTTGCATCAGTGCAATTAAGGAGTTCGAGCAGGTGCCCGGA
 CACTTGACTGATGACTCCAGCTGTCTCCCTTAGGACCTGGTGCAGATCAGAAAGGGCTGTGCGCACTT
 TACTCAAGGACATTTCTGAAGCTTCCCTTGCACTGTGGCTGGGCTGTGAGCTGTCTCAAGGAAAGGGCTTT
 ATTTGTGAATTTGCCAGAAACGACTGTGATCTTCCCATTTCCAGACAGCAACATGTAGAAAGATTTCCAGC
 GTTGGAGGGCTTGTCTTCAAAACAGCTGTCTCCAGCTCTCCAGCAACATGATGCCCTGAGTACTGTGAAAGAGCTGT
 GGAGAAACCTTCTGGAAAGTGTGGCTCTCCAGCAACATGATGCCCTGAGTACTGTGAAAGAGCTGTCT
 AACATGCCCTTATGATAACCCGATTTGTGTCTATTATTGGTGACATGTTTTAGATATTGGGATTGTATA
 TTAAAGCAGCAGGGCTGATAGTTGTGGTTTTGTTTACAAATGTTCTGTTTTGGCTGCTATTGGTTTTTAA
 GAGGTTTTTATACCTTTGTATTGATAGTATGTTTCACTGATGCTGAGGCCAGTTTGTATGTGTGTGCA
 TATATTGTGAAGTGTACTGCAAGAGTGAATTACTCAGTTTCTCTTTCTCTAAAGCTTGTGTTAGAACTG
 GTTGGTCTTTCTAGTGMANAAANATATGACCCCAAAAAAAAAAAAAAAAAAAGCAATGCGAAGGTG
 CTATCTCAGGCTGTGTGTGGCCGCTTGCAGCTTCTGTCTGAGCAGCAATGGGCGACAAAGGAAGA
 CAGGCGCTCGCCACCCTGTCTGAGCGCGAACCCGCG

FIGURE 46

GGAAATTATAGATCTTGATTTGAATCCATCAGTGATTCAGAGATACACCTATTTGCCATAAACACCTA
 ACATGATTTGGTTATGGAATCATGTGTTGGATAGGTTCTTAAAGCTGTTTCCCTCAAATCTTGACACAGTT
 TTCAGAGGGGCTTAAAGTACTTGCACGGTTGGGCAGTAAATCCAGATTTACCTAAGATTTGGGTAAAAAGT
 CATCTGTGACTTAAAGTCTGGCAGGGCATTGCTAAGTGGAGTACAGGATCTAAAGGGGTTTTCTTAGAAGGG
 CAAATTTGTCCAAATGNGTAGCAGCAAGGACTCTGGGTTAGAAAGCATCTGCACAAAACTGGTGAGACCTA
 CTTCTCACCTCTCCAGCTGCAGCTGGATGGCTGATGSCAGGCTGAGCAGTGGGGAGCAGGTTTTAAACACAGG
 AGTCLTTCAGGCTCACTGTATATTGAGNAGAAACATAAACTATTGTCTGTACATTCGAGGTCAGCGCTT
 CTCTTACGCTTTTATAATATGCAAAATGCCAGCTTCTGGAAAGCAGTATCATCATGTAACCAATGCTTTA
 TACACCATCATCATGTAATTTTATGATGCTCAGAACTTGTGTAATATGTCTCTTAGATGATTTTGG
 GGAGATGTCTATTATTTTCATATTTCAAATGCAATTTCAATTAAGATTTATCTATTGAGACAAAC
 GAAAAA

FIGURE 47

AATTTTGGCCCCCGGAAGGCCAAGAAATTTCCGGCCACCGANGGAATTTTGGTACCACCCAGGGGG
 GAAATTCGAATGCTGCTTCNAACCTAGCTTCCCTTCCATTCTCTAGTCTGSCCTTTGACACAAAT
 CTGGTAGAAGTAAGCCTGATAAATTGAGGGCACTGTACCTCCCTTGGCCCCGAGAAGGCTCTGGGAGG
 AAGTCCAGCAATTTGTAACACGGCGGGTGGAGGGCGGGTGGATGGCCATGGGCTGGCCCTGCGTATCAGGC
 CTGCTCACCATTCTGGAGCTTATTCTGATCTCAATTTGAATGTCAGAGGGAGCATATNAGGCCCA
 GAGCTCCGATTTCCAAAGATGATATTGACATTTATGGAGATTGGTGTGTAACATATTTTGAATAATACT
 AACTTATTTTGGTGGGGTTTGGTTGCTCTGTCTTAGGACCTGTAGTATTGTTGCTGATTTTTC
 CGTTATTTCTACATAGGCCAAGAGAATTGGAGGGATAGACAGCTCCAAGAAAAGTGAAGTGGTGGGAGA
 GAATGGCTTTTTCCTTTTCTTTTCTTCTTAGTTTTCTTCTGGCTGAGATTCGTCGACAGACAGCA
 CCAATAGACATTTAGAGTTGACATTTGACATTTAATGGGGCCATGCTCATTTTGTAGATTGACAGAG
 TGGCTTCCCTCCCTGCTCCAACTCCATCAGACAGGGTGTGACAGCTGGGAGTCTGGGCTCTTCCACGG
 AGAGGCTCTAATGCTGGACACAGAGCACGGCTAGGCTGGGAGGGATGGGAGCCATGGCCCCCTCTTGA
 GAGCGGGCTTCCGTTAGGAAGGACAGTGGGGGTGCTGCTGATATAGTTTCACTGGTCACTGCTT
 TATGAGTAGTGTTTTGTGCACTGCCAGGGTTTTCCTCTGTGTGGAGGGGATGATTGAAGCAATGG
 TGTCTGGAGTAAGCCTTACAAATTTAATAGACTTTTCTTATCATATCCCTCATTTCTTCCCTGAATAA
 AATACACACAGCAAAAAAATATGATAGTTTACATCTCTTAGTTCCCTTGGCCAAACAGAAATATTCT
 TAGTTCCACTGGCCAGGATTTTCTACATAGTCAGAACTTACACATTACTAGAGGCACACCCACAGGAG
 TATTGTCTTCACTTTTATCTGTGACACAGCCAAATACCCACATTGGAAGAGCCCATTTGTGATGGGTAA
 ACATCCCTCTCTGCTCCCAACACCCCTGTGACTGCTGCTCATGTGTTCACTGACCTCCGAGGCCCTAAT
 CATGAAGCAGCAAAACCCAGAGATCTCCACCCCTGCTCAGGAGCTTCTGTGAAGAGGGGATGAAGTG
 GGTCTCCAGGAGGAGCAGTGGGGGCTTGTGGCAGCTGGCTCGGGAGCCGGCTTACAGGAGGGCAGCTCTG
 CAGTTGGGAGGGGACCGTCCCGAGGAGACAGGCTCTACACACCCCACTCTACTATCATCTCTGCT
 CACACACCTTGTCCAAGGCTTTATGCACTGGATTTATTTTCCAAATCGAGGAGCAGGTAGATGATCAT
 TTTCCCGAGGCTGTCTGAGAAAGGTGGCTAAATGTATACTGTTGTCAGAAATGCTGAGATCTCCCCCACT
 TTTGGTTTGTGACAGTAAAACTCTTTCACATGTGACTTATTTTCTCTCAGGACAGCCAGCCACCTGG
 TCCCCTGTGTGACTCTAGACAGTGGCCAGGATCCAATAGAGTCCAGGGGTGACCGCAGGATGGTGGG
 GCAGCGGGCTTCTCACTACCCAGCCACCAAGGCCCTGACGCATGCTCCTGCACTCTCAGACATATC
 CTGTGACACGCTGGAGGGTGCATGGCCCGCTCACCCTTGTTCAGATGGTGGAAACGCTGATGATACAG
 CTCTTCCCTGGCTGCCCTGCCAGGAGCAGGCAATGTGAACTGGCTGGTGTTCGACCTCCAGCGGCA
 TGGCTCCAGCCCAACCCACAGTGGAGACTGGAGCAGGGCAATGAGTCTGGTGGGGGACCTGGACATG
 CCCCATAGGGGGCCCCACCCAGACTTAACAGGCAAGTCTCTGGGCTTGGCCGACGAGGACTCAATGCTAA
 AGCAAGCTGCTGGCTGCTGTGCCAGGGCCCCCTCTCTGATTTACATCCCATTTTACACAGACCCCTC
 CTCTTTAATAAAGCTGACAGTTCTGTGGCAGCCAGAAACCCACACCATGAAGACAGGAGATGGGGGCC
 TTTGTGCCCACTCCAGCACGCTGCTGTCTGGGGTGTGTGAGAGGATGTTGCTGTCTGTGGCTGGTGG
 TCTGCTGAGACGTTCCGAGGACGGGGAATTCAGGGGTGGTGGGGGCTGAGGCTTATATGTGAACATGA
 TGCAGAGTTGCGCTGCAGAGGATCTGGATATACATATGTAATAATTGTACGTGTAATTTAAATATATC
 TGTGTGCAATCGCTATGAGAAATATATGTAAGGCTCTGAAGGAGAGGGAGATGTACATCTTCCGACAG
 TCTTGGGAGGCTTATGCCAGTCAATGAATGATGAGTGTGATCCAGTGGTGCAGAAAGCTACATCCATG
 TGTCACTACGCTTATGACTCTTAATGTATTTTAAAGCAAAAAATGTCAGCGACCTCAGCTTCAACGCTG
 GATTTCTCGAGTCCAGCTTTCTGTGCCAGTGTCTCACTGAGCCACAGCCTCTCGCATCTGGGAGCCGCG
 TGGCTCGGCTCTCGGGGACAGTTGCCATGGAGCCCTCTGGGCTCATTCACAAATGTGCTGAGTGGCA
 CTGTGAACCCCTGAGAGAGTGGAGTCTTGGCCAGCTTAAGAGAAAGATTTCTCAGGGTATTTATTA
 GTGTGTCCACAGGCTCAGAGACAGATGGAAGATGCTTCACTGCTGTAATTTATTAACAGGCAAA
 GATTTTGTGTTTCTTGATGACAGACTTAAAGTTGGGAGCTTATTTCCATTTGAGAAAGTATAAATAT
 ATTPAAGATGATACCTTCTCTGCTTAAGTTGCTGCTTCACTGCTCAATGAGTTTAAGGAGCAATGAGTAT
 ATGATACCAATGAGGGTTGGTTATTAATCAACCTGAATAGGCTGTGGTTCTCCAGCAATATTTCTCTGT
 ACTCAACATGGAGCCATATTAAGAGTGTGTGTTTATATGATACATTTGTGATATTTTGTCTGTGT
 TGAATGTTCTTTCTAATAGTTTCTTATGTTTCTTAAAGTGTGATGATGATGATGATGATGATGATGAT
 TAACTGCAATACAGGTGGCTCTGCTGGGTCTCTGCTGCTTTATTTACTTTAAGGACAGTGTGATGAT
 TGGTCCACACGCTTTCAAAAAATGGAACCTGCCCTGCCCTCCCCCTTTGCTGACACAGCTGTACTATG
 ACCACTTCTACCATCATTTATGCTGTGAATAACAACTCTTTGTGGTGCATTTATCTCATGCTCTGCCAA
 TCTGATATATATCTATGGCTTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 48